#12

```
  1   GACAGAGTGCAGCCTTTTCAGACTCTGTGACACAGTTCCCCTTTT
 46   GCAAAAATACTTAGCGAGGATCATTACTTTCCAACAGTCGTGTCC
 91   AGAGACCTACTTTGTAACACCGCAGGGAAGTTAATGTACTAGGTC
136   TTGAAAGGTCTTTCTGGAATGTGCAGTAACTTGTAGTTTTCTTCT
181   AGTAGCACTGCTAATTTTTGTGTTATAATTTTTGTAGGTCCATGG

226   GGCCGATGTATGGGAGATGAATGTGGTCCCGGAGGCATCCAAACG
                 MetGlyAspGluCysGlyProGlyGlyIleGlnThr

271   AGGGCTGTGTGGTGTGCTCATGTGGAGGGATGGACTACACTGCAT
      ArgAlaValTrpCysAlaHisValGluGlyTrpThrThrLeuHis

316   ACTAACTGTAAGCAGGCCGAGAGACCCAATAACCAGCAGAATTGT
      ThrAsnCysLysGlnAlaGluArgProAsnAsnGlnGlnAsnCys

361   TTCAAAGTTTGCGATTGGCACAAAGAGTTGTACGACTGGAGACTG
      PheLysValCysAspTrpHisLysGluLeuTyrAspTrpArgLeu

406   GGACCTTGGAATCAGTGTCAGCCCGTGATTTCAAAAAGCCTAGAG
      GlyProTrpAsnGlnCysGlnProValIleSerLysSerLeuGlu

451   AAACCTCTTGAGTGCATTAAGGGGGAAGAAGGTATTCAGGTGAGG
      LysProLeuGluCysIleLysGlyGluGluGlyIleGlnValArg

496   GAGATAGCGTGCATCCAGAAAGACAAAGACATTCCTGCGGAGGAT
      GluIleAlaCysIleGlnLysAspLysAspIleProAlaGluAsp

541   ATCATCTGTGAGTACTTTGAGCCCAAGCCTCTCCTGGAGCAGGCT
      IleIleCysGluTyrPheGluProLysProLeuLeuGluGlnAla

586   TGCCTCATTCCTTGCCAGCAAGATTGCATCGTGTCTGAATTTTCT
      CysLeuIleProCysGlnGlnAspCysIleValSerGluPheSer

631   GCCTGGTCCGAATGCTCCAAGACCTGCGGCAGCGGGCTCCAGCAC
      AlaTrpSerGluCysSerLysThrCysGlySerGlyLeuGlnHis

676   CGGACGCGTCATGTGGTGGCGCCCCCGCAGTTCGGAGGCTCTGGC
      ArgThrArgHisValValAlaProProGlnPheGlyGlySerGly

721   TGTCCAAACCTGACGGAGTTCCAGGTGTGCCAATCCAGTCCATGC
      CysProAsnLeuThrGluPheGlnValCysGlnSerSerProCys

766   GAGGCCGAGGAGCTCAGGTACAGCCTGCATGTGGGGCCCTGGAGC
      GluAlaGluGluLeuArgTyrSerLeuHisValGlyProTrpSer

811   ACCTGCTCAATGCCCCACTCCCGACAAGTAAGACAAGCAAGGAGA
      ThrCysSerMetProHisSerArgGlnValArgGlnAlaArgArg
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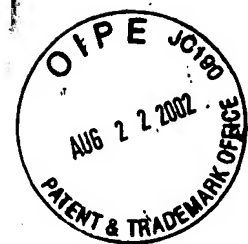
Fig 1

856 CGCGGGAAGAATAAAGAACGGGAAAAGGACCGCAGCAAAGGAGTA
     ArgGlyLysAsnLysGluArgGluLysAspArgSerLysGlyVal

901 AAGGATCCAGAAGCCCGCGAGCTTATTAAGAAAAAGAGAAACAGA
     LysAspProGluAlaArgGluLeuIleLysLysLysArgAsnArg

946 AACAGGCAGAACAGACAAGAGAACAAATATTGGGACATCCAGATT
     AsnArgGlnAsnArgGlnGluAsnLysTyrTrpAspIleGlnIle

991 GGATATCAGACCAGAGAGGTTATGTGCATTAACAAGACGGGGAAA
     GlyTyrGlnThrArgGluValMetCysIleAsnLysThrGlyLys

1036 GCTGCTGATTTAAGCTTTTGCCAGCAAGAGAAGCTTCCAATGACC
     AlaAlaAspLeuSerPheCysGlnGlnGluLysLeuProMetThr

1081 TTCCAGTCCTGTGTGATCACCAAAGAGTGCCAGGTTTCCGAGTGG
     PheGlnSerCysValIleThrLysGluCysGlnValSerGluTrp

1126 TCAGAGTGGAGCCCCTGCTCAAAAACATGCCATGACATGGTGTCC
     SerGluTrpSerProCysSerLysThrCysHisAspMetValSer

1171 CCTGCAGGCACTCGTGTAAGGACACGAACCATCAGGCAGTTTCCC
     ProAlaGlyThrArgValArgThrArgThrIleArgGlnPhePro

1216 ATTGGCAGTGAAAAGGAGTGTCCAGAATTTGAAGAAAAGAACCC
     IleGlySerGluLysGluCysProGluPheGluGluLysGluPro

1261 TGTTTGTCTCAAGGAGATGGAGTTGTCCCCTGTGCCACGTATGGC
     CysLeuSerGlnGlyAspGlyValValProCysAlaThrTyrGly

1306 TGGAGAACTACAGAGTGGACTGAGTGCCGTGTGGACCCTTTGCTC
     TrpArgThrThrGluTrpThrGluCysArgValAspProLeuLeu

1351 AGTCAGCAGGACAAGAGGCGCGGCAACCAGACGGCCCTCTGTGGA
     SerGlnGlnAspLysArgArgGlyAsnGlnThrAlaLeuCysGly

1396 GGGGGCATCCAGACCCGAGAGGTGTACTGCGTGCAGGCCAACGAA
     GlyGlyIleGlnThrArgGluValTyrCysValGlnAlaAsnGlu

1441 AACCTCCTCTCACAATTAAGTACCCACAAGAACAAAGAAGCCTCA
     AsnLeuLeuSerGlnLeuSerThrHisLysAsnLysGluAlaSer

1486 AAGCCAATGGACTTAAAATTATGCACTGGACCTATCCCTAATACT
     LysProMetAspLeuLysLeuCysThrGlyProIleProAsnThr

1531 ACACAGCTGTGCCACATTCCTTGTCCAACTGAATGTGAAGTTTCA
     ThrGlnLeuCysHisIleProCysProThrGluCysGluValSer

Fig 1 (continued)

1576   CCTTGGTCAGCTTGGGGACCTTGTACTTATGAAAACTGTAATGAT
ProTrpSerAlaTrpGlyProCysThrTyrGluAsnCysAsnAsp

1621   CAGCAAGGGAAAAAAGGCTTCAAACTGAGGAAGCGGCGCATTACC
GlnGlnGlyLysLysGlyPheLysLeuArgLysArgArgIleThr

1666   AATGAGCCCACTGGAGGCTCTGGGGTAACCGGAAACTGCCCTCAC
AsnGluProThrGlyGlySerGlyValThrGlyAsnCysProHis

1711   TTACTGGAAGCCATTCCCTGTGAAGAGCCTGCCTGTTATGACTGG
LeuLeuGluAlaIleProCysGluGluProAlaCysTyrAspTrp

1756   AAAGCGGTGAGACTGGGAGACTGCGAGCCAGATAACGGAAAGGAG
LysAlaValArgLeuGlyAspCysGluProAspAsnGlyLysGlu

1801   TGTGGTCCAGGCACGCAAGTTCAAGAGGTTGTGTGCATCAACAGT
CysGlyProGlyThrGlnValGlnGluValValCysIleAsnSer

1846   GATGGAGAAGAAGTTGACAGACAGCTGTGCAGAGATGCCATCTTC
AspGlyGluGluValAspArgGlnLeuCysArgAspAlaIlePhe

1891   CCCATCCCTGTGGCCTGTGATGCCCCATGCCCGAAAGACTGTGTG
ProIleProValAlaCysAspAlaProCysProLysAspCysVal

1936   CTCAGCACATGGTCTACGTGGTCCTCCTGCTCACACACCTGCTCA
LeuSerThrTrpSerThrTrpSerSerCysSerHisThrCysSer

1981   GGGAAAACGACAGAAGGGAAACAGATACGAGCACGATCCATTCTG
GlyLysThrThrGluGlyLysGlnIleArgAlaArgSerIleLeu

2026   GCCTATGCGGGTGAAGAAGGTGGAATTCGCTGTCCAAATAGCAGT
AlaTyrAlaGlyGluGluGlyGlyIleArgCysProAsnSerSer

2071   GCTTTGCAAGAAGTACGAAGCTGTAATGAGCATCCTTGCACAGTG
AlaLeuGlnGluValArgSerCysAsnGluHisProCysThrVal

2116   TACCACTGGCAAACTGGTCCCTGGGGCCAGTGCATTGAGGACACC
TyrHisTrpGlnThrGlyProTrpGlyGlnCysIleGluAspThr

2161   TCAGTATCGTCCTTCAACACAACTACGACTTGGAATGGGGAGGCC
SerValSerSerPheAsnThrThrThrThrTrpAsnGlyGluAla

2206   TCCTGCTCTGTCGGCATGCAGACAAGAAAAGTCATCTGTGTGCGA
SerCysSerValGlyMetGlnThrArgLysValIleCysValArg

2251   GTCAATGTGGGCCAAGTGGGACCCAAAAAATGTCCTGAAAGCCTT
ValAsnValGlyGlnValGlyProLysLysCysProGluSerLeu

Fig 1 (continued)

2296 CGACCTGAAACTGTAAGGCCTTGTCTGCTTCCTTGTAAGAAGGAC
ArgProGluThrValArgProCysLeuLeuProCysLysLysAsp

2341 TGTATTGTGACCCCATATAGTGACTGGACATCATGCCCCTCTTCG
CysIleValThrProTyrSerAspTrpThrSerCysProSerSer

2386 TGTAAAGAAGGGGACTCCAGTATCAGGAAGCAGTCTAGGCATCGG
CysLysGluGlyAspSerSerIleArgLysGlnSerArgHisArg

2431 GTCATCATTCAGCTGCCAGCCAACGGGGGCCGAGACTGCACAGAT
ValIleIleGlnLeuProAlaAsnGlyGlyArgAspCysThrAsp

2476 CCCCTCTATGAAGAGAAGGCCTGTGAGGCACCTCAAGCGTGCCAA
ProLeuTyrGluGluLysAlaCysGluAlaProGlnAlaCysGln

2521 AGCTACAGGTGGAAGACTCACAAATGGCGCAGATGCCAATTAGTC
SerTyrArgTrpLysThrHisLysTrpArgArgCysGlnLeuVal

2566 CCTTGGAGCGTGCAACAAGACAGCCCTGGAGCACAGGAAGGCTGT
ProTrpSerValGlnGlnAspSerProGlyAlaGlnGluGlyCys

2611 GGGCCTGGGCGACAGGCAAGAGCCATTACTTGTCGCAAGCAAGAT
GlyProGlyArgGlnAlaArgAlaIleThrCysArgLysGlnAsp

2656 GGAGGACAGGCTGGAATCCATGAGTGCCTACAGTATGCAGGCCCT
GlyGlyGlnAlaGlyIleHisGluCysLeuGlnTyrAlaGlyPro

2701 GTGCCAGCCCTTACCCAGGCCTGCCAGATCCCCTGCCAGGATGAC
ValProAlaLeuThrGlnAlaCysGlnIleProCysGlnAspAsp

2746 TGTCAATTGACCAGCTGGTCCAAGTTTTCTTCATGCAATGGAGAC
CysGlnLeuThrSerTrpSerLysPheSerSerCysAsnGlyAsp

2791 TGTGGTGCAGTTAGGACCAGAAAGCGCACTCTTGTTGGAAAAAGT
CysGlyAlaValArgThrArgLysArgThrLeuValGlyLysSer

2836 AAAAAGAAGGAAAAATGTAAAAATTCCCATTTGTATCCCCTGATT
LysLysLysGluLysCysLysAsnSerHisLeuTyrProLeuIle

2881 GAGACTCAGTATTGTCCTTGTGACAAATATAATGCACAACCTGTG
GluThrGlnTyrCysProCysAspLysTyrAsnAlaGlnProVal

2926 GGGAACTGGTCAGACTGTATTTTACCAGAGGGAAAAGTGGAAGTG
GlyAsnTrpSerAspCysIleLeuProGluGlyLysValGluVal

2971 TTGCTGGGAATGAAAGTACAAGGAGACATCAAGGAATGCGGACAA
LeuLeuGlyMetLysValGlnGlyAspIleLysGluCysGlyGln

Fig 1 (continued)

3016   GGATATCGTTACCAAGCAATGGCATGCTACGATCAAAATGGCAGG
GlyTyrArgTyrGlnAlaMetAlaCysTyrAspGlnAsnGlyArg

3061   CTTGTGGAAACATCTAGATGTAACAGCCATGGTTACATTGAGGAG
LeuValGluThrSerArgCysAsnSerHisGlyTyrIleGluGlu

3106   GCCTGCATCATCCCCTGCCCCTCAGACTGCAAGCTCAGTGAGTGG
AlaCysIleIleProCysProSerAspCysLysLeuSerGluTrp

3151   TCCAACTGGTCGCGCTGCAGCAAGTCCTGTGGGAGTGGTGTGAAG
SerAsnTrpSerArgCysSerLysSerCysGlySerGlyValLys

3196   GTTCGTTCTAAATGGCTGCGTGAAAAACCATATAATGGAGGAAGG
ValArgSerLysTrpLeuArgGluLysProTyrAsnGlyGlyArg

3241   CCTTGCCCCAAACTGGACCATGTCAACCAGGCACAGGTGTATGAG
ProCysProLysLeuAspHisValAsnGlnAlaGlnValTyrGlu

3286   GTTGTCCCATGCCACAGTGACTGCAACCAGTACCTATGGGTCACA
ValValProCysHisSerAspCysAsnGlnTyrLeuTrpValThr

3331   GAGCCCTGGAGCATCTGCAAGGTGACCTTTGTGAATATGCGGGAG
GluProTrpSerIleCysLysValThrPheValAsnMetArgGlu

3376   AACTGTGGAGAGGGCGTGCAAACCCGAAAAGTGAGATGCATGCAG
AsnCysGlyGluGlyValGlnThrArgLysValArgCysMetGln

3421   AATACAGCAGATGGCCCTTCTGAACATGTAGAGGATTACCTCTGT
AsnThrAlaAspGlyProSerGluHisValGluAspTyrLeuCys

3466   GACCCAGAAGAGATGCCCCTGGGCTCTAGAGTGTGCAAATTACCA
AspProGluGluMetProLeuGlySerArgValCysLysLeuPro

3511   TGCCCTGAGGACTGTGTGATATCTGAATGGGGTCCATGGACCCAA
CysProGluAspCysValIleSerGluTrpGlyProTrpThrGln

3556   TGTGTTTTGCCTTGCAATCAAAGCAGTTTCCGGCAAAGGTCAGCT
CysValLeuProCysAsnGlnSerSerPheArgGlnArgSerAla

3601   GATCCCATCAGACAACCAGCTGATGAAGGAAGATCTTGCCCTAAT
AspProIleArgGlnProAlaAspGluGlyArgSerCysProAsn

3646   GCTGTTGAGAAGAACCCTGTAACCTGAACAAAAACTGCTACCAC
AlaValGluLysGluProCysAsnLeuAsnLysAsnCysTyrHis

3691   TATGATTATAATGTAACAGACTGGAGTACATGTCAGCTGAGTGAG
TyrAspTyrAsnValThrAspTrpSerThrCysGlnLeuSerGlu

Fig 1 (continued)

3736 AAGGCAGTTTGTGGAAATGGAATAAAAACAAGGATGTTGGATTGT
LysAlaValCysGlyAsnGlyIleLysThrArgMetLeuAspCys

3781 GTTCGAAGTGATGGCAAGTCAGTTGACCTGAAATATTGTGAAGCG
ValArgSerAspGlyLysSerValAspLeuLysTyrCysGluAla

3826 CTTGGCTTGGAGAAGAACTGGCAGATGAACACGTCCTGCATGGTG
LeuGlyLeuGluLysAsnTrpGlnMetAsnThrSerCysMetVal

3871 GAATGCCCTGTGAACTGTCAGCTTTCTGATTGGTCTCCTTGGTCA
GluCysProValAsnCysGlnLeuSerAspTrpSerProTrpSer

3916 GAATGTTCTCAAACATGTGGCCTCACAGGAAAAATGATCCGAAGA
GluCysSerGlnThrCysGlyLeuThrGlyLysMetIleArgArg

3961 CGAACAGTGACCCAGCCCTTTCAAGGTGATGGAAGACCATGCCCT
ArgThrValThrGlnProPheGlnGlyAspGlyArgProCysPro

4006 TCCCTGATGGACCAGTCCAAACCCTGCCCAGTGAAGCCTTGTTAT
SerLeuMetAspGlnSerLysProCysProValLysProCysTyr

4051 CGGTGGCAATATGGCCAGTGGTCTCCATGCCAAGTGCAGGAGGCC
ArgTrpGlnTyrGlyGlnTrpSerProCysGlnValGlnGluAla

4096 CAGTGTGGAGAAGGGACCAGAACAAGGAACATTTCTTGTGTAGTA
GlnCysGlyGluGlyThrArgThrArgAsnIleSerCysValVal

4141 AGTGATGGGTCAGCTGATGATTTCAGCAAAGTGGTGGATGAGGAA
SerAspGlySerAlaAspAspPheSerLysValValAspGluGlu

4186 TTCTGTGCTGACATTGAACTCATTATAGATGGTAATAAAAATATG
PheCysAlaAspIleGluLeuIleIleAspGlyAsnLysAsnMet

4231 GTTCTGGAGGAATCCTGCAGCCAGCCTTGCCCAGGTGACTGTTAT
ValLeuGluGluSerCysSerGlnProCysProGlyAspCysTyr

4276 TTGAAGGACTGGTCTTCCTGGAGCCTGTGTCAGCTGACCTGTGTG
LeuLysAspTrpSerSerTrpSerLeuCysGlnLeuThrCysVal

4321 AATGGTGAGGATCTAGGCTTTGGTGGAATACAGGTCAGATCCAGA
AsnGlyGluAspLeuGlyPheGlyGlyIleGlnValArgSerArg

4366 CCGGTGATTATACAAGAACTAGAGAATCAGCATCTGTGCCCAGAG
ProValIleIleGlnGluLeuGluAsnGlnHisLeuCysProGlu

4411 CAGATGTTAGAAACAAAATCATGTTATGATGGACAGTGCTATGAA
GlnMetLeuGluThrLysSerCysTyrAspGlyGlnCysTyrGlu

4456 TATAAATGGATGGCCAGTGCTTGGAAGGGCTCTTCCCGAACAGTG
TyrLysTrpMetAlaSerAlaTrpLysGlySerSerArgThrVal

Fig 1 (continued)

4501   TGGTGTCAAAGGTCAGATGGTATAAATGTAACAGGGGGCTGCTTG
        TrpCysGlnArgSerAspGlyIleAsnValThrGlyGlyCysLeu

4546   GTGATGAGCCAGCCTGATGCCGACAGGTCTTGTAACCCACCGTGT
        ValMetSerGlnProAspAlaAspArgSerCysAsnProProCys

4591   AGTCAACCCCACTCGTACTGTAGCGAGACAAAAACATGCCATTGT
        SerGlnProHisSerTyrCysSerGluThrLysThrCysHisCys

4636   GAAGAAGGGTACACTGAAGTCATGTCTTCTAACAGCACCCTTGAG
        GluGluGlyTyrThrGluValMetSerSerAsnSerThrLeuGlu

4681   CAATGCACACTTATCCCCGTGGTGGTATTACCCACCATGGAGGAC
        GlnCysThrLeuIleProValValValLeuProThrMetGluAsp

4726   AAAAGAGGAGATGTGAAAACCAGTCGGGCTGTACATCCAACCCAA
        LysArgGlyAspValLysThrSerArgAlaValHisProThrGln

4771   CCCTCCAGTAACCCAGCAGGACGGGGAAGGACCTGGTTTCTACAG
        ProSerSerAsnProAlaGlyArgGlyArgThrTrpPheLeuGln

4816   CCATTTGGGCCAGATGGGAGACTAAAGACCTGGGTTTACGGTGTA
        ProPheGlyProAspGlyArgLeuLysThrTrpValTyrGlyVal

4861   GCAGCTGGGGCATTTGTGTTACTCATCTTTATTGTCTCCATGATT
        AlaAlaGlyAlaPheValLeuLeuIlePheIleValSerMetIle

4906   TATCTAGCTTGCAAAAAGCCAAAGAAACCCCAAAGAAGGCAAAAC
        TyrLeuAlaCysLysLysProLysLysProGlnArgArgGlnAsn

4951   AACCGACTGAAACCTTTAACCTTAGCCTATGATGGAGATGCCGAC
   AsnArgLeuLysProLeuThrLeuAlaTyrAspGlyAspAlaAsp

4996   ATGTAACATATAACTTTTCCTGGCAACAACCAGTTTCGGCTTTCT
        Met

Fig 1 (continued)

```
5041   GACTTCATAGATGTCCAGAGGCCACAACAAATGTATCCAAACTGT
5086   GTGGATTAAAATATATTTTAATTTTTAAAAATGGCATCATAAAGA
5131   CAAGAGTGAAAATCATACTGCCACTGGAGATATTTAAGACAGTAC
5176   CACTTATATACAGACCATCAACCGTGAGAATTATAGGAGATTTAG
5221   CTGAATACATGCTGCATTCTGAAAGTTTTATGTCATCTTTTCTGA
5266   AATCTACCGACTGAAAAACCACTTTCATCTCTAAAAAATAATGGT
5311   GGAATTGGCCAGTTAGGATGCCTGATACAAGACCGTCTGCAGTGT
5356   TAATCCATAAAACTTCCTAGCATGAAGAGTTTCTACCAAGATCTC
5401   CACAATACTATGGTCAAATTAACATGTGTACTCAGTTGAATGACA
5446   CACATTATGTCAGATTATGTACTTGCTAATAAGCAATTTTAACAA
5491   TGCATAACAAATAAACTCTAAGCTAAGCAGAAAATCCACTGAATA
5536   AATTCAGCATCTTGGTGGTCGATGGTAGATTTTATTGACCTGCAT
5581   TTCAGAGACAAAGCCTCTTTTTTAAGACTTCTTGTCTCTCTCCAA
5626   AGTAAGAATGCTGGACAAGTACTAGTGTCTTAGAAGAACGAGTCC
5671   TCAAGTTCAGTATTTTATAGTGGTAATTGTCTGGAAAACTAATTT
5716   ACTTGTGTTAATACAATACGTTTCTACTTTCCCTGATTTTCAAAC
5761   TGGTTGCCTGCATCTTTTTTGCTATATGGAAGGCACATTTTTGCA
5806   CTATATTAGTGCAGCACGATAGGCGCTTAACCAGTATTGCCATAG
5851   AAACTGCCTCTTTTCATGTGGGATGAAGACATCTGTGCCAAGAGT
5896   GGCATGAAGACATTTGCAAGTTCTTGTATCCTGAAGAGAGTAAAG
5941   TTCAGTTTGGATGGCAGCAAGATGAAATCAGCTATTACACCTGCT
5986   GTACACACACTTCCTCATCACTGCAGCCATTGTGAAATTGACAAC
6031   ATGGCGGTAATTTAAGTGTTGAAGTCCCTAACCCCTTAACCCTCT
6076   AAAAGGTGGATTCCTCTAGTTGGTTTGTAATTGTTCTTTGAAGGC
6121   TGTTTATGACTAGATTTTTATATTTGTTATCTTTGTTAAGAAAAA
6166   AAAAAGAAAAAGGAACTGGATGTCTTTTTAATTTTGAGCAGATGG
6211   AGAAAATAAATAATGTATCAATGACCTTTGTAACTAAAGGAAAAA
6256   AAAAAAAAATGTGGATTTTCCTTTCTCTCTGATTTCCCAGTTTCA
6301   GATTGAATGTCTGTCTTGCAGGCAGTTATTTCAAAATCCATAGTC
6346   TTTNGCCTTTCTCACTGGCAAAATTTGA
```

Fig 1 (continued)
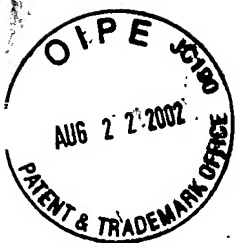
```
   1   CACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCCCCTTTGGAG
  46   CCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCAGTGATGGTA
  91   AGTGCTGGCCCAGACTGAAGCTCGGAGAGGCACTCTGCTTGCCCA
 136   GCGTCACAGTCTTAGCTCCCAACTGTCCTGGCTTCCAGTCTCCCT
 181   TGCTTCCCAGATCCCAGACTCTAGCCCCAGCCCCGTCTCTTTCAC
 226   CAGCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTC
 271   GCCCCACATGTAACTGTATCTACAACCAGCTGCACCAGCGACACC
 316   TGTCCAACCCGGCCCGGCCTGGGATGCTATGTGGGGGCCCCCAGC
 361   CTGGGGTGCAGGGCCCCTGTCAGGTCTGATAGGGAGAAGAGAAGG
 406   AGCAGAAGGGGAGGGGCCTAACCCTGGGCTGGGGGTTGGACTCAC
 451   AGGACTGGGGGAAAGAGCTGCAATCAGAGGGTGTCTGCCATAGCT
 496   GGGCTCAGGCATCTGTCCTTGGCTTTGTTGCCTGGCTCCAGGGAG
 541   ATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGG
 586   TTCAGGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGG
 631   ACGCTCCTGTGCTGCTGACCAACACAGCTGCTCACAGTTCCTGGC
 676   TGCAGGCTCGAGTTCAGGGGGCAGCTTTCCTGGCCCAGAGCCCAG

 721   AGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGAT
              MetSerAspGluAspSerCysValAlaCysGlyS

 766   CCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCCTCCCCATGGC
       erLeuArgThrAlaGlyProGlnAlaGlyAlaProSerProTrpP

 811   CCTGGGAGGCCAGGCTGATGCACCAGGGACAGCTGGCCTGTGGCG
       roTrpGluAlaArgLeuMetHisGlnGlyGlnLeuAlaCysGlyG

 856   GAGCCCTGGTGTCAGAGGAGGCGGTGCTAACTGCTGCCCACTGCT
       lyAlaLeuValSerGluGluAlaValLeuThrAlaAlaHisCysP

 901   TCAATGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGA
       heAsnGlyArgGlnAlaProGluGluTrpSerValGlyLeuGlyT

 946   CCAGACCGGAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAG
       hrArgProGluGluTrpGlyLeuLysGlnLeuIleLeuHisGlyA

 991   CCTACACCCACCCTGAGGGGGGCTACGACATGGCCCTCCTGCTGC
       laTyrThrHisProGluGlyGlyTyrAspMetAlaLeuLeuLeuL

1036   TGGCTCAGCCTGTGACACTGGGAGCCAGCCTGCGGGCCCTCTGCC
       euAlaGlnProValThrLeuGlyAlaSerLeuArgAlaLeuCysL

1081   TGCCCTATTTTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGG
       euProTyrPheAspHisHisLeuProAspGlyGluArgGlyTrpV

1126   TTCTGGGACGGGCCCGCCCAGGAGCAGGCATCAGCTCCCTCCAGA
       alLeuGlyArgAlaArgProGlyAlaGlyIleSerSerLeuGlnT

1171   CAGTGCCCGTGACCCTCCTGGGGCCTAGGGCCTGCAGCCGGCTGC
       hrValProValThrLeuLeuGlyProArgAlaCysSerArgLeuH
```

Fig. 2

1216   ATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGG
        isAlaAlaProGlyGlyAspGlySerProIleLeuProGlyMetV

1261   TGTGTACCAGTGCTGTGGGTGAGCTGCCCAGCTGTGAGGGCCTGT
        alCysThrSerAlaValGlyGluLeuProSerCysGluGlyLeuS

1306   CTGGGGCACCACTGGTGCATGAGGTGAGGGGCACATGGTTCCTGG
        erGlyAlaProLeuValHisGluValArgGlyThrTrpPheLeuA

1351   CCGGGCTGCACAGCTTCGGAGATGCTTGCCAAGGCCCCGCCAGGC
        laGlyLeuHisSerPheGlyAspAlaCysGlnGlyProAlaArgP

1396   CGGCGGTCTTCACCGCGCTCCCTGCCTATGAGGACTGGGTCAGCA
        roAlaValPheThrAlaLeuProAlaTyrGluAspTrpValSerS

1441   GTTTGGACTGGCAGGTCTACTTCGCCGAGGAACCAGAGCCCGAGG
        erLeuAspTrpGlnValTyrPheAlaGluGluProGluProGluA

1486   CTGAGCCTGGAAGCTGCCTGGCCAACATAAGCCAACCAACCAGCT
        laGluProGlySerCysLeuAlaAsnIleSerGlnProThrSerC

1531   GCTGACAGGGGACCTGGCCATTCTCAGGACAAGAGAATGCAGGCA
        ys

1576   GGCAAATGGCATTACTGCCCCTGTCCTCCCCACCCTGTCATGTGT
1621   GATTCCAGGCACCAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGA
1666   AGGAACCTGCCTGGGGCCACAGGTGCCCCCTCCCCACCCTGCAGG
1711   ACAGGGGTGTCTGTGGACACTCCCACACCCAACTCTGCTACCAAG
1756   CAGGCGTCTCAGCTTTCCTCCTCCTTTACCCTTTCAGATACAATC
1801   ACGCCAGCCCCGTTGTTTGAAAATTTCTTTTTTTGGGGGGCAGC
1846   AGTTTTCCTTTTTTTAAACTTAAATAAATTGTTACAAAATAGACT
1891   TTAG

Fig. 2 (continued)

```
  1   GCGGATCCTCACACGACTGTGATCCGATTCTTTCCAGCGGCTTCT
 46   GCAACCAAGCGGGTCTTACCCCCGGTCCTCCGCGTCTCCAGTCCT
 91   CGCACCTGGAACCCCAACGTCCCCGAGAGTCCCCGAATCCCCGCT

136   CCCAGGCTACCTAAGAGGATGAGCGGTGCTCCGACGGCCGGGGCA
                         MetSerGlyAlaProThrAlaGlyAla

181   GCCCTGATGCTCTGCGCCGCCACCGCCGTGCTACTGAGCGCTCAG
      AlaLeuMetLeuCysAlaAlaThrAlaValLeuLeuSerAlaGln

226   GGCGGACCCGTGCAGTCCAAGTCGCCGCGCTTTGCGTCCTGGGAC
      GlyGlyProValGlnSerLysSerProArgPheAlaSerTrpAsp

271   GAGATGAATGTCCTGGCGCACGGACTCCTGCAGCTCGGCCAGGGG
      GluMetAsnValLeuAlaHisGlyLeuLeuGlnLeuGlyGlnGly

316   TGCGCGAACACCGGAGCGCACCCGCAGTCAGCTGAGCGCGCTGGA
      CysAlaAsnThrGlyAlaHisProGlnSerAlaGluArgAlaGly

361   GCGCGCCTGAGCGCGTGCGGGTCCGCCTGTCAGGGAACCGAGGGG
      AlaArgLeuSerAlaCysGlySerAlaCysGlnGlyThrGluGly

406   TCCACCGACCTCCCGTTAGCCCCTGAGAGCCGGGTGGACCCTGAG
      SerThrAspLeuProLeuAlaProGluSerArgValAspProGlu

451   GTCCTTCACAGCCTGCAGACACAACTCAAGGCTCAGAACAGCAGG
      ValLeuHisSerLeuGlnThrGlnLeuLysAlaGlnAsnSerArg

496   ATCCAGCAACTCTTCCACAAGGTGGCCCAGCAGCAGCGGCACCTG
      IleGlnGlnLeuPheHisLysValAlaGlnGlnGlnArgHisLeu

541   GAGAAGCAGCACCTGCGAATTCAGCATCTGCAAAGCCAGTTTGGC
      GluLysGlnHisLeuArgIleGlnHisLeuGlnSerGlnPheGly

586   CTCCTGGACCACAAGCACCTAGACCATGAGGTGGCCAAGCCTGCC
      LeuLeuAspHisLysHisLeuAspHisGluValAlaLysProAla

631   CGAAGAAAGAGGCTGCCCGAGATGGCCCAGCCAGTTGACCCGGCT
      ArgArgLysArgLeuProGluMetAlaGlnProValAspProAla

676   CACAATGTCAGCCGCCTGCACCGGCTGCCCAGGGATTGCCAGGAG
      HisAsnValSerArgLeuHisArgLeuProArgAspCysGlnGlu

721   CTGTTCCAGGTTGGGGAGAGGCAGAGTGGACTATTTGAAATCCAG
      LeuPheGlnValGlyGluArgGlnSerGlyLeuPheGluIleGln

766   CCTCAGGGGTCTCCGCCATTTTTTGGTGAACTGCAAGATGACCTCA
      ProGlnGlySerProProPheLeuValAsnCysLysMetThrSer
```

Fig. 3

```
 811   GATGGAGGCTGGACAGTAATTCAGAGGCGCCACGATGGCTCAGTG
       AspGlyGlyTrpThrValIleGlnArgArgHisAspGlySerVal

 856   GACTTCAACCGGCCCTGGGAAGCCTACAAGGCGGGGTTTGGGGAT
       AspPheAsnArgProTrpGluAlaTyrLysAlaGlyPheGlyAsp

 901   CCCCACGGCGAGTTCTGGCTGGGTCTGGAGAAGGTGCATAGCATG
       ProHisGlyGluPheTrpLeuGlyLeuGluLysValHisSerMet

 946   ATGGGGGACCGCAACAGCCGCCTGGCCGTGCAGCTGCGGGACTGG
       MetGlyAspArgAsnSerArgLeuAlaValGlnLeuArgAspTrp

 991   GATGGCAACGCCGAGTTGCTGCAGTTCTCCGTGCACCTGGGTGGC
       AspGlyAsnAlaGluLeuLeuGlnPheSerValHisLeuGlyGly

1036   GAGGACACGGCCTATAGCCTGCAGCTCACTGCACCCGTGGCCGGC
       GluAspThrAlaTyrSerLeuGlnLeuThrAlaProValAlaGly

1081   CAGCTGGGCGCCACCACCGTCCCACCCAGCGGCCTCTCCGTACCC
       GlnLeuGlyAlaThrThrValProProSerGlyLeuSerValPro

1126   TTCTCCACTTGGGACCAGGATCACGACCTCCGCAGGGACAAGAAC
       PheSerThrTrpAspGlnAspHisAspLeuArgArgAspLysAsn

1171   TGCGCCAAGAGCCTCTCTGGAGGCTGGTGGTTTGGCACCTGCAGC
       CysAlaLysSerLeuSerGlyGlyTrpTrpPheGlyThrCysSer

1216   CATTCCAACCTCAACGGCCAGTACTTCCGCTCCATCCCACAGCAG
       HisSerAsnLeuAsnGlyGlnTyrPheArgSerIleProGlnGln

1261   CGGCAGAAGCTTAAGAAGGGAATCTTCTGGAAGACCTGGCGGGGC
       ArgGlnLysLeuLysLysGlyIlePheTrpLysThrTrpArgGly

1306   CGCTACTACCCGCTGCAGGCCACCACCATGTTGATCCAGCCCATG
       ArgTyrTyrProLeuGlnAlaThrThrMetLeuIleGlnProMet

1351   GCAGCAGAGGCAGCCTCCTAGCGTCCTGGCTGGGCCTGGTCCCAG
       AlaAlaGluAlaAlaSer

1396   GCCCACGAAAGACGGTGACTCTTGGCTCTGCCCGAGGATGTGGCC
1441   GTTCCCTGCCTGGGCAGGGGCTCCAAGGAGGGGCCATCTGGAAAC
1486   TTGTGGACAGAGAAGAAGACCACGACTGGAGAAGCCCCCTTTCTG
1531   AGTGCAGGGGGGCTGCATGCGTTGCCTCCTGAGATCGAGGCTGCA
1576   GGATATGCTCAGACTCTAGAGGCGTGGACCAAGGGGCATGGAGCT
1621   TCACTCCTTGCTGGCCAGGGAGTTGGGGACTCAGAGGGACCACTT
1666   GGGGCCAGCCAGACTGGCCTCAATGGCGGACTCAGTCACATTGAC
1711   TGACGGGGACCAGGGCTTGTGTGGGTCGAGAGCGCCCTCATGGTG
1756   CTGGTGCTGTTGTGTGTAGGTCCCCTGGGGACACAAGCAGGCGCC
1801   AATGGTATCTGGGCGGAGCTCACAGAGTTCTTGGAATAAAAGCAA
1846   CCTCAGAACA
```

Fig. 3 (continued)

1   GGTAGCCGACGCGCCGGCCGGCGCGTGACCTTGCCCCTCTTGCTC

46   GCCTTGAAAATGGAAAAGATGCTCGCAGGCTGCTTTCTGCTGATC
               MetGluLysMetLeuAlaGlyCysPheLeuLeuIle

91   CTCGGACAGATCGTCCTCCTCCCTGCCGAGGCCAGGGAGCGGTCA
       LeuGlyGlnIleValLeuLeuProAlaGluAlaArgGluArgSer

136   CGTGGGAGGTCCATCTCTAGGGGCAGACACGCTCGGACCCACCCG
       ArgGlyArgSerIleSerArgGlyArgHisAlaArgThrHisPro

181   CAGACGGCCCTTCTGGAGAGTTCCTGTGAGAACAAGCGGGCAGAC
       GlnThrAlaLeuLeuGluSerSerCysGluAsnLysArgAlaAsp

226   CTGGTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGAC
       LeuValPheIleIleAspSerSerArgSerValAsnThrHisAsp

271   TATGCAAAGGTCAAGGAGTTCATCGTGGACATCTTGCAATTCTTG
       TyrAlaLysValLysGluPheIleValAspIleLeuGlnPheLeu

316   GACATTGGTCCTGATGTCACCCGAGTGGGCCTGCTCCAATATGGC
       AspIleGlyProAspValThrArgValGlyLeuLeuGlnTyrGly

361   AGCACTGTCAAGAATGAGTTCTCCCTCAAGACCTTCAAGAGGAAG
       SerThrValLysAsnGluPheSerLeuLysThrPheLysArgLys

406   TCCGAGGTGGAGCGTGCTGTCAAGAGGATGCGGCATCTGTCCACG
       SerGluValGluArgAlaValLysArgMetArgHisLeuSerThr

451   GGCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCA
       GlyThrMetThrGlyLeuAlaIleGlnTyrAlaLeuAsnIleAla

496   TTCTCAGAAGCAGAGGGGGCCCGGCCCCTGAGGGAGAATGTGCCA
       PheSerGluAlaGluGlyAlaArgProLeuArgGluAsnValPro

541   CGGGTCATAATGATCGTGACGGATGGGAGACCTCAGGACTCCGTG
       ArgValIleMetIleValThrAspGlyArgProGlnAspSerVal

586   GCCGAGGTGGCTGCTAAGGCACGGGACACGGGCATCCTAATCTTT
       AlaGluValAlaAlaLysAlaArgAspThrGlyIleLeuIlePhe

631   GCCATTGGTGTGGGCCAGGTAGACTTCAACACCTTGAAGTCCATT
       AlaIleGlyValGlyGlnValAspPheAsnThrLeuLysSerIle

676   GGGAGTGAGCCCCATGAGGACCATGTCTTCCTTGTGGCCAATTTC
       GlySerGluProHisGluAspHisValPheLeuValAlaAsnPhe

721   AGCCAGATTGAGACGCTGACCTCCGTGTTCCAGAAGAAGTTGTGC
       SerGlnIleGluThrLeuThrSerValPheGlnLysLysLeuCys

Fig. 4

766   ACGGCCCACATGTGCAGCACCCTGGAGCATAACTGTGCCCACTTC
           ThrAlaHisMetCysSerThrLeuGluHisAsnCysAlaHisPhe

811   TGCATCAACATCCCTGGCTCATACGTCTGCAGGTGCAAACAAGGC
           CysIleAsnIleProGlySerTyrValCysArgCysLysGlnGly

856   TACATTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTG
           TyrIleLeuAsnSerAspGlnThrThrCysArgIleGlnAspLeu

901   TGTGCCATGGAGGACCACAACTGTGAGCAGCTCTGTGTGAATGTG
           CysAlaMetGluAspHisAsnCysGluGlnLeuCysValAsnVal

946   CCGGGCTCCTTCGTCTGCGAGTGCTACAGTGGCTACGCCCTGGCT
           ProGlySerPheValCysGluCysTyrSerGlyTyrAlaLeuAla

991   GAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCTCAGAA
           GluAspGlyLysArgCysValAlaValAspTyrCysAlaSerGlu

1036   AACCACGGATGTGAACATGAGTGTGTAAATGCTGATGGCTCCTAC
           AsnHisGlyCysGluHisGluCysValAsnAlaAspGlySerTyr

1081   CTTTGCCAGTGCCATGAAGGATTTGCTCTTAACCCAGATGAAAAA
           LeuCysGlnCysHisGluGlyPheAlaLeuAsnProAspGluLys

1126   ACGTGCACAAAGATAGACTACTGTGCCTCATCTAATCATGGATGT
           ThrCysThrLysIleAspTyrCysAlaSerSerAsnHisGlyCys

1171   CAGTACGAGTGTGTTAACACAGATGATTCCTATTCCTGCCACTGC
           GlnTyrGluCysValAsnThrAspAspSerTyrSerCysHisCys

1216   CTGAAAGGCTTTACCCTGAATCCAGATAAGAAAACCTGCAGAAGG
           LeuLysGlyPheThrLeuAsnProAspLysLysThrCysArgArg

1261   ATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGC
           IleAsnTyrCysAlaLeuAsnLysProGlyCysGluHisGluCys

1306   GTCAACATGGAGGAGAGCTACTACTGCCGCTGCCACCGTGGCTAC
           ValAsnMetGluGluSerTyrTyrCysArgCysHisArgGlyTyr

1351   ACTCTGGACCCCAATGGCAAACCCTGCAGCCGAGTGGACCACTGT
           ThrLeuAspProAsnGlyLysProCysSerArgValAspHisCys

1396   GCACAGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAG
           AlaGlnGlnAspHisGlyCysGluGlnLeuCysLeuAsnThrGlu

1441   GATTCCTTCGTCTGCCAGTGCTCAGAAGGCTTCCTCATCAACGAG
           AspSerPheValCysGlnCysSerGluGlyPheLeuIleAsnGlu

Fig. 4 (continued)

1486   GACCTCAAGACCTGCTCCCGGGTGGATTACTGCCTGCTGAGTGAC
        AspLeuLysThrCysSerArgValAspTyrCysLeuLeuSerAsp

1531   CATGGTTGTGAATACTCCTGTGTCAACATGGACAGATCCTTTGCC
        HisGlyCysGluTyrSerCysValAsnMetAspArgSerPheAla

1576   TGTCAGTGTCCTGAGGGACACGTGCTCCGCAGCGATGGGAAGACG
        CysGlnCysProGluGlyHisValLeuArgSerAspGlyLysThr

1621   TGTGCAAAATTGGACTCTTGTGCTCTGGGGGACCACGGTTGTGAA
        CysAlaLysLeuAspSerCysAlaLeuGlyAspHisGlyCysGlu

1666   CATTCGTGTGTAAGCAGTGAAGATTCGTTTGTGTGCCAGTGCTTT
        HisSerCysValSerSerGluAspSerPheValCysGlnCysPhe

1711   GAAGGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAA
        GluGlyTyrIleLeuArgGluAspGlyLysThrCysArgArgLys

1756   GATGTCTGCCAAGCTATAGACCATGGCTGTGAACACATTTGTGTG
        AspValCysGlnAlaIleAspHisGlyCysGluHisIleCysVal

1801   AACAGTGACGACTCATACACGTGCGAGTGCTTGGAGGGATTCCGG
        AsnSerAspAspSerTyrThrCysGluCysLeuGluGlyPheArg

1846   CTCACTGAGGATGGGAAACGCTGCCGAATTTCCTCAGGGAAGGAT
        LeuThrGluAspGlyLysArgCysArgIleSerSerGlyLysAsp

1891   GTCTGCAAATCAACCCACCATGGCTGCGAACACATTTGTGTTAAT
        ValCysLysSerThrHisHisGlyCysGluHisIleCysValAsn

1936   AATGGGAATTCCTACATCTGCAAATGCTCAGAGGGATTTGTTCTA
        AsnGlyAsnSerTyrIleCysLysCysSerGluGlyPheValLeu

1981   GCTGAGGACGGAAGACGGTGCAAGAAATGCACTGAAGGCCCAATT
        AlaGluAspGlyArgArgCysLysLysCysThrGluGlyProIle

2026   GACCTGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAG
        AspLeuValPheValIleAspGlySerLysSerLeuGlyGluGlu

2071   AATTTTGAGGTCGTGAAGCAGTTTGTCACTGGAATTATAGATTCC
        AsnPheGluValValLysGlnPheValThrGlyIleIleAspSer

2116   TTGACAATTTCCCCCAAAGCCGCTCGAGTGGGGCTGCTCCAGTAT
        LeuThrIleSerProLysAlaAlaArgValGlyLeuLeuGlnTyr

2161   TCCACACAGGTCCACACAGAGTTCACTCTGAGAAACTTCAACTCA
        SerThrGlnValHisThrGluPheThrLeuArgAsnPheAsnSer

2206   GCCAAAGACATGAAAAAAGCCGTGGCCCACATGAAATACATGGGA
        AlaLysAspMetLysLysAlaValAlaHisMetLysTyrMetGly

Fig. 4 (continued)

2251 AAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAGAGA
     LysGlySerMetThrGlyLeuAlaLeuLysHisMetPheGluArg

2296 AGTTTTACCCAAGGAGAAGGGGCCAGGCCCCTTTTCCACAAGGGT
     SerPheThrGlnGlyGluGlyAlaArgProLeuPheHisLysGly

2341 GCCCAGAGCAGCCATTGTGTTCACCGACGGACGGGCTCAGGATGA
     AlaGlnSerSerHisCysValHisArgArgThrGlySerGly

2386 CGTCTCCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTAT
2431 GTATGCTGTTGGGGTAGGAAAAGCCATTGAGGAGGAACTACAAGA
2476 GATTGCCTCTGAGCCCACAAACAAGCATCTCTTCTATGCCGAAGA
2521 CTTCAGCACAATGGATGAGATAAGTGAAAAACTCAAGAAAGGCAT
2566 CTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAGC
2611 AGGGGAACTGCCAAAAACGGTCCAACAGCCAACAGAATCTGAGCC
2656 AGTCACCATAAATATCCAAGACCTACTTTCCTGTTCTAATTTTGC
2701 AGTGCAACACAGATATCTGTTTGAAGAAGACAATCTTTTACGGTC
2746 TACACAAAGCTTTCCCATTCAACAAAACCTTCAGGAAGCCCTTT
2791 GGAAGAAAAACACGATCAATGCAAATGTGAAAACCTTATAATGTT
2836 CCAGAACCTTGCAAACGAAGAAGTAAGAAAATTTACACAGCGCTT
2881 AGAAGAAATGACACAGAGAATGGAAGCCCTGGAAAATCGCCTGAG
2926 ATACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCATTGTA
2971 TCACGGATTACAATGAACGCAGTGCAGAGCCCCAAAGCTCAGGCT
3016 ATTGTTAAATC

Fig. 4 (continued)

```
  1  GGTAGCCGACGCGCCGGCCGGCGCGTGACCTTGCCCCTCTTGCTC

 46  GCCTTGAAAATGGAAAAGATGCTCGCAGGCTGCTTTCTGCTGATC
        MetGluLysMetLeuAlaGlyCysPheLeuLeuIle

 91  CTCGGACAGATCGTCCTCCTCCCCTGCGAGGCCAGGGAGCGGTCA
     LeuGlyGlnIleValLeuLeuProCysGluAlaArgGluArgSer

136  CGTGGGAGGTCCATCTCTAGGGGCAGACACGCTCGGACCCACCCG
     ArgGlyArgSerIleSerArgGlyArgHisAlaArgThrHisPro

181  CAGACGGCCCTTCTGGAGAGTTCCTGTGAGAACAAGCGGGCAGAC
     GlnThrAlaLeuLeuGluSerSerCysGluAsnLysArgAlaAsp

226  CTGGTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGAC
     LeuValPheIleIleAspSerSerArgSerValAsnThrHisAsp

271  TATGCAAAGGTCAAGGAGTTCATCGTGGACATCTTGCAATTCTTG
     TyrAlaLysValLysGluPheIleValAspIleLeuGlnPheLeu

316  GACATTGGTCCTGATGTCACCCGAGTGGGCCTGCTCCAATATGGC
     AspIleGlyProAspValThrArgValGlyLeuLeuGlnTyrGly

361  AGCACTGTCAAGAATGAGTTCTCCCTCAAGACCTTCAAGAGGAAG
     SerThrValLysAsnGluPheSerLeuLysThrPheLysArgLys

406  TCCGAGGTGGAGCGTGCTGTCAAGAGGATGCGGCATCTGTCCACG
     SerGluValGluArgAlaValLysArgMetArgHisLeuSerThr

451  GGCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCA
     GlyThrMetThrGlyLeuAlaIleGlnTyrAlaLeuAsnIleAla

496  TTCTCAGAAGCAGAGGGGGGCCCGGCCCCTGAGGGAGAATGTGCCA
     PheSerGluAlaGluGlyAlaArgProLeuArgGluAsnValPro

541  CGGGTCATAATGATCGTGACGGATGGGAGACCTCAGGACTCCGTG
     ArgValIleMetIleValThrAspGlyArgProGlnAspSerVal

586  GCCGAGGTGGCTGCTAAGGCACGGGACACGGGCATCCTAATCTTT
     AlaGluValAlaAlaLysAlaArgAspThrGlyIleLeuIlePhe

631  GCCATTGGTGTGGGCCAGGTAGACTTCAACACCTTGAAGTCCATT
     AlaIleGlyValGlyGlnValAspPheAsnThrLeuLysSerIle

676  GGGAGTGAGCCCCATGAGGACCATGTCTTCCTTGTGGCCAATTTC
     GlySerGluProHisGluAspHisValPheLeuValAlaAsnPhe

721  AGCCAGATTGAGACGCTGACCTCCGTGTTCCAGAAGAAGTTGTGC
     SerGlnIleGluThrLeuThrSerValPheGlnLysLysLeuCys
```

Fig. 5

766 ACGGCCCACATGTGCAGCACCCTGGAGCATAACTGTGCCCACTTC
     ThrAlaHisMetCysSerThrLeuGluHisAsnCysAlaHisPhe

811 TGCATCAACATCCCTGGCTCATACGTCTGCAGGTGCAAACAAGGC
     CysIleAsnIleProGlySerTyrValCysArgCysLysGlnGly

856 TACATTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTG
     TyrIleLeuAsnSerAspGlnThrThrCysArgIleGlnAspLeu

901 TGTGCCATGGAGGACCACAACTGTGAGCAGCTCTGTGTGAATGTG
     CysAlaMetGluAspHisAsnCysGluGlnLeuCysValAsnVal

946 CCGGGCTCCTTCGTCTGCGAGTGCTACAGTGGCTACGCCCTGGCT
     ProGlySerPheValCysGluCysTyrSerGlyTyrAlaLeuAla

991 GAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCTCAGAA
     GluAspGlyLysArgCysValAlaValAspTyrCysAlaSerGlu

1036 AACCACGGATGTGAACATGAGTGTGTAAATGCTGATGGCTCCTAC
     AsnHisGlyCysGluHisGluCysValAsnAlaAspGlySerTyr

1081 CTTTGCCAGTGCCATGAAGGATTTGCTCTTAACCCAGATGAAAAA
     LeuCysGlnCysHisGluGlyPheAlaLeuAsnProAspGluLys

1126 ACGTGCACAAAGATAGACTACTGTGCCTCATCTAATCATGGATGT
     ThrCysThrLysIleAspTyrCysAlaSerSerAsnHisGlyCys

1171 CAGTACGAGTGTGTTAACACAGATGATTCCTATTCCTGCCACTGC
     GlnTyrGluCysValAsnThrAspAspSerTyrSerCysHisCys

1216 CTGAAAGGCTTTACCCTGAATCCAGATAAGAAAACCTGCAGAAGG
     LeuLysGlyPheThrLeuAsnProAspLysLysThrCysArgArg

1261 ATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGC
     IleAsnTyrCysAlaLeuAsnLysProGlyCysGluHisGluCys

1306 GTCAACATGGAGGAGAGCTACTACTGCCGCTGCCACCGTGGCTAC
     ValAsnMetGluGluSerTyrTyrCysArgCysHisArgGlyTyr

1351 ACTCTGGACCCCAATGGCAAACCCTGCAGCCGAGTGGACCACTGT
     ThrLeuAspProAsnGlyLysProCysSerArgValAspHisCys

1396 GCACAGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAG
     AlaGlnGlnAspHisGlyCysGluGlnLeuCysLeuAsnThrGlu

1441 GATTCCTTCGTCTGCCAGTGCTCAGAAGGCTTCCTCATCAACGAG
     AspSerPheValCysGlnCysSerGluGlyPheLeuIleAsnGlu

1486 GACCTCAAGACCTGCTCCCGGGTGGATTACTGCCTGCTGAGTGAC
     AspLeuLysThrCysSerArgValAspTyrCysLeuLeuSerAsp

Fig. 5 (continued)

1531   CATGGTTGTGAATACTCCTGTGTCAACATGGACAGATCCTTTGCC
       HisGlyCysGluTyrSerCysValAsnMetAspArgSerPheAla

1576   TGTCAGTGTCCTGAGGGACACGTGCTCCGCAGCGATGGGAAGACG
       CysGlnCysProGluGlyHisValLeuArgSerAspGlyLysThr

1621   TGTGCAAAATTGGACTCTTGTGCTCTGGGGGACCACGGTTGTGAA
       CysAlaLysLeuAspSerCysAlaLeuGlyAspHisGlyCysGlu

1666   CATTCGTGTGTAAGCAGTGAAGATTCGTTTGTGTGCCAGTGCTTT
       HisSerCysValSerSerGluAspSerPheValCysGlnCysPhe

1711   GAAGGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAA
       GluGlyTyrIleLeuArgGluAspGlyLysThrCysArgArgLys

1756   GATGTCTGCCAAGCTATAGACCATGGCTGTGAACACATTTGTGTG
       AspValCysGlnAlaIleAspHisGlyCysGluHisIleCysVal

1801   AACAGTGACGACTCATACACGTGCGAGTGCTTGGAGGGATTCCGG
       AsnSerAspAspSerTyrThrCysGluCysLeuGluGlyPheArg

1846   CTCACTGAGGATGGGAAACGCTGCCGAATTTCCTCAGGGAAGGAT
       LeuThrGluAspGlyLysArgCysArgIleSerSerGlyLysAsp

1891   GTCTGCAAATCAACCCACCATGGCTGCGAACACATTTGTGTTAAT
       ValCysLysSerThrHisHisGlyCysGluHisIleCysValAsn

1936   AATGGGAATTCCTACATCTGCAAATGCTCAGAGGGATTTGTTCTA
       AsnGlyAsnSerTyrIleCysLysCysSerGluGlyPheValLeu

1981   GCTGAGGACGGAAGACGGTGCAAGAAATGCACTGAAGGCCCAATT
       AlaGluAspGlyArgArgCysLysLysCysThrGluGlyProIle

2026   GACCTGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAG
       AspLeuValPheValIleAspGlySerLysSerLeuGlyGluGlu

2071   AATTTTGAGGTCGTGAAGCAGTTTGTCACTGGAATTATAGATTCC
       AsnPheGluValValLysGlnPheValThrGlyIleIleAspSer

2116   TTGACAATTTCCCCCAAAGCCGCTCGAGTGGGGCTGCTCCAGTAT
       LeuThrIleSerProLysAlaAlaArgValGlyLeuLeuGlnTyr

2161   TCCACACAGGTCCACACAGAGTTCACTCTGAGAAACTTCAACTCA
       SerThrGlnValHisThrGluPheThrLeuArgAsnPheAsnSer

2206   GCCAAAGACATGAAAAAAGCCGTGGCCCACATGAAATACATGGGA
       AlaLysAspMetLysLysAlaValAlaHisMetLysTyrMetGly

Fig. 5 (continued)

2251 AAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAGAGA
     LysGlySerMetThrGlyLeuAlaLeuLysHisMetPheGluArg

2296 AGTTTTACCCAAGGAGAAGGGGCCAGGCCCTTTTCCACAAGGGTG
     SerPheThrGlnGlyGluGlyAlaArgProPheSerThrArgVal

2341 CCCAGAGCAGCCATTGTGTTCACCGACGGACGGGCTCAGGATGAC
     ProArgAlaAlaIleValPheThrAspGlyArgAlaGlnAspAsp

2386 GTCTCCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATG
     ValSerGluTrpAlaSerLysAlaLysAlaAsnGlyIleThrMet

2431 TATGCTGTTGGGGTAGGAAAAGCCATTGAGGAGGAACTACAAGAG
     TyrAlaValGlyValGlyLysAlaIleGluGluGluLeuGlnGlu

2476 ATTGCCTCTGAGCCCACAAACAAGCATCTCTTCTATGCCGAAGAC
     IleAlaSerGluProThrAsnLysHisLeuPheTyrAlaGluAsp

2521 TTCAGCACAATGGATGAGATAAGTGAAAAACTCAAGAAAGGCATC
     PheSerThrMetAspGluIleSerGluLysLeuLysLysGlyIle

2566 TGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAGCA
     CysGluAlaLeuGluAspSerAspGlyArgGlnAspSerProAla

2611 GGGGAACTGCCAAAAACGGTCCAACAGCCAACAGAATCTGAGCCA
     GlyGluLeuProLysThrValGlnGlnProThrGluSerGluPro

2656 GTCACCATAAATATCCAAGACCTACTTTCCTGTTCTAATTTTGCA
     ValThrIleAsnIleGlnAspLeuLeuSerCysSerAsnPheAla

2701 GTGCAACACAGATATCTGTTTGAAGAAGACAATCTTTTACGGTCT
     ValGlnHisArgTyrLeuPheGluGluAspAsnLeuLeuArgSer

2746 ACACAAAAGCTTTCCCATTCAACAAAACCTTCAGGAAGCCCTTTG
     ThrGlnLysLeuSerHisSerThrLysProSerGlySerProLeu

2791 GAAGAAAAACACGATCAATGCAAATGTGAAAACCTTATAATGTTC
     GluGluLysHisAspGlnCysLysCysGluAsnLeuIleMetPhe

2836 CAGAACCTTGCAAACGAAGAAGTAAGAAAATTAACACAGCGCTTA
     GlnAsnLeuAlaAsnGluGluValArgLysLeuThrGlnArgLeu

2881 GAAGAAATGACACAGAGAATGGAAGCCCTGGAAAATCGCCTGAGA
     GluGluMetThrGlnArgMetGluAlaLeuGluAsnArgLeuArg

2926 TACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCATTGTAT
     TyrArg

Fig. 5 (continued)

```
2971   CACGGATTACAATGAACGCAGTGCAGAGCCCCAAAGCTCAGGCTA
3016   TTGTTAAATCAATAATGTTGTGAAGTAAAACAATCAGTACTGAGA
3061   AACCTGGTTTGCCACAGAACAAAGACAAGAAGTATACACTAACTT
3106   GTATAAATTTATCTAGGAAAAAAATCCTTCAGAATTCTAAGATGA
3151   ATTTACCAGGTGAGAATGAATAAGCTATGCAAGGTATTTTGTAAT
3196   ATACTGTGGACACAACTTGCTTCTGCCTCATCCTGCCTTAGTGTG
3241   CAATCTCATTTGACTATACGATAAAGTTTGCACAGTCTTACTTCT
3286   GTAGAACACTGGCCATAGGAAATGCTGTTTTTTTGTACTGGACTT
3331   TACCTTGATATATGTATATGGATGTATGCATAAAATCATAGGACA
3376   TATGTACTTGTGGAACAAGTTGGATTTTTTATACAATATTAAAAT
3421   TCACCACTTCAGAGAAAAGTAAAAAAA
```

Fig. 5 (continued)

```
  1 CGGCCCTTCTCACACTCCTGCCCTGCTGATGTGGAACGGGGTTTG
 46 GGGTTCTGCAGGGCTATTGTCTGCGCTGGGGAAGGGGACAGGCCG
 91 GGACCGGGACCTCCGCTCGCAGCCGGCCGCACCAGCAGGACAGCT

136 GGCCTGAAGCTCAGAGCCGGGGCGTGCGCCATGGCCCCACACTGG
                                 MetAlaProHisTrp

181 GCTGTCTGGCTGCTGGCAGCAAGGCTGTGGGGCCTGGGCATTGGG
    AlaValTrpLeuLeuAlaAlaArgLeuTrpGlyLeuGlyIleGly

226 GCTGAGGTGTGGTGGAACCTTGTGCCGCGTAAGACAGTGTCTTCT
    AlaGluValTrpTrpAsnLeuValProArgLysThrValSerSer

271 GGGGAGCTGGCCACGGTAGTACGGCGGTTCTCCCAGACCGGCATC
    GlyGluLeuAlaThrValValArgArgPheSerGlnThrGlyIle

316 CAGGACTTCCTGACACTGACGCTGACGGAGCCCACTGGGCTTCTG
    GlnAspPheLeuThrLeuThrLeuThrGluProThrGlyLeuLeu

361 TACGTGGGCGCCCGAGAGGCCCTGTTTGCCTTCAGCATGGAGGCC
    TyrValGlyAlaArgGluAlaLeuPheAlaPheSerMetGluAla

406 CTGGAGCTGCAAGGAGCGATCTCCTGGGAGGCCCCCGTGGAGAAG
    LeuGluLeuGlnGlyAlaIleSerTrpGluAlaProValGluLys

451 AAGACTGAGTGTATCCAGAAAGGGAAGAACAACCAGACCGAGTGC
    LysThrGluCysIleGlnLysGlyLysAsnAsnGlnThrGluCys

496 TTCAACTTCATCCGCTTCCTGCAGCCCTACAATGCCTCCCACCTG
    PheAsnPheIleArgPheLeuGlnProTyrAsnAlaSerHisLeu

541 TACGTCTGTGGCACCTACGCCTTCCAGCCCAAGTGCACCTACGTC
    TyrValCysGlyThrTyrAlaPheGlnProLysCysThrTyrVal

586 AACATGCTCACCTTCACTTTGGAGCATGGAGAGTTTGAAGATGGG
    AsnMetLeuThrPheThrLeuGluHisGlyGluPheGluAspGly

631 AAGGGCAAGTGTCCCTATGACCCAGCTAAGGGCCATGCTGGCCTT
    LysGlyLysCysProTyrAspProAlaLysGlyHisAlaGlyLeu

676 CTTGTGGATGGTGAGCTGTACTCGGCCACACTCAACAACTTCCTG
    LeuValAspGlyGluLeuTyrSerAlaThrLeuAsnAsnPheLeu

721 GGCACGGAACCCATTATCCTGCGTAACATGGGGCCCCACCACTCC
    GlyThrGluProIleIleLeuArgAsnMetGlyProHisHisSer
```

Fig. 6

766 ATGAAGACAGAGTACCTGGCCTTTTGGCTCAACGAACCTCACTTT
    MetLysThrGluTyrLeuAlaPheTrpLeuAsnGluProHisPhe

811 GTAGGCTCTGCCTATGTACCTGAGAGGGTGGGCCTGCTGTGGACA
    ValGlySerAlaTyrValProGluArgValGlyLeuLeuTrpThr

856 ATGGCATACTCTCTTCCAGCCCTAGGAGGAGGGCTCCTAACAGTG
    MetAlaTyrSerLeuProAlaLeuGlyGlyGlyLeuLeuThrVal

901 TAACTTATTGTGTCCCCGCGTATTTATTTGTTGTAAATATTTGAG
946 TATTTTTATATTGACAAATAAA

Fig. 6 (continued)

```
  1   GGCACCAGGCCTTCCGGAGAGACGCAGTCGGCTGCCACCCCGGGA
                                                  M

 46   TGGGTCGCTGGTGCCAGACCGTCGCGCGCGGGCAGCGCCCCCGGA
      etGlyArgTrpCysGlnThrValAlaArgGlyGlnArgProArgT

 91   CGTCTGCCCCCTCCCGCGCCGGTGCCCTGCTGCTGCTGCTTCTGT
      hrSerAlaProSerArgAlaGlyAlaLeuLeuLeuLeuLeuLeuL

136   TGCTGAGGTCTGCAGGTTGCTGGGGCGCAGGGGAAGCCCCGGGGG
      euLeuArgSerAlaGlyCysTrpGlyAlaGlyGluAlaProGlyA

181   CGCTGTCCACTGCTGATCCCGCCGACCAGAGCGTCCAGTGTGTCC
      laLeuSerThrAlaAspProAlaAspGlnSerValGlnCysValP

226   CCAAGGCCACCTGTCCTTCCAGCCGGCCTCGCCTTCTCTGGCAGA
      roLysAlaThrCysProSerSerArgProArgLeuLeuTrpGlnT

271   CCCCGACCACCCAGACACTGCCCTCGACCACCATGGAGACCCAAT
      hrProThrThrGlnThrLeuProSerThrThrMetGluThrGlnP

316   TCCCAGTTTCTGAAGGCAAAGTCGACCCATACCGCTCCTGTGGCT
      heProValSerGluGlyLysValAspProTyrArgSerCysGlyP

361   TTTCCTACGAGCAGGACCCCACCCTCAGGGACCCAGAAGCCGTGG
      heSerTyrGluGlnAspProThrLeuArgAspProGluAlaValA

406   CTCGGCGGTGGCCCTGGATGGTCAGCGTGCGGGCCAATGGCACAC
      laArgArgTrpProTrpMetValSerValArgAlaAsnGlyThrH

451   ACATCTGTGCCGGCACCATCATTGCCTCCCAGTGGGTGCTGACTG
      isIleCysAlaGlyThrIleIleAlaSerGlnTrpValLeuThrV

496   TGGCCCACTGCCTGATCTGGCGTGATGTTATCTACTCAGTGAGGG
      alAlaHisCysLeuIleTrpArgAspValIleTyrSerValArgV

541   TGGGGAGTCCGTGGATTGACCAGATGACGCAGACCGCCTCCGATG
      alGlySerProTrpIleAspGlnMetThrGlnThrAlaSerAspV

586   TCCCCGGTGCTCCAGGTCATCATGCATAGCAGGTACCGGGCCCAGC
      alProValLeuGlnValIleMetHisSerArgTyrArgAlaGlnA

631   GGTTCTGGTCCTGGGTGGGCCAGGCCAACGACATCGGCCTCCTCA
      rgPheTrpSerTrpValGlyGlnAlaAsnAspIleGlyLeuLeuL

676   AGCTCAAGCAGGAACTCAAGTACAGCAATTACGTGCGGCCCATCT
      ysLeuLysGlnGluLeuLysTyrSerAsnTyrValArgProIleC
```

Fig. 7

721 GCCTGCCTGGCACGGACTATGTGTTGAAGGACCATTCCCGCTGCA
ysLeuProGlyThrAspTyrValLeuLysAspHisSerArgCysT

766 CTGTGACGGGCTGGGGACTTTCCAAGGCTGACGGCATGTGGCCTC
hrValThrGlyTrpGlyLeuSerLysAlaAspGlyMetTrpProG

811 AGTTCCGGACCATTCAGGAGAAGGAAGTCATCATCCTGAACAACA
lnPheArgThrIleGlnGluLysGluValIleIleLeuAsnAsnL

856 AAGAGTGTGACAATTTCTACCACAACTTCACCAAAATCCCCACTC
ysGluCysAspAsnPheTyrHisAsnPheThrLysIleProThrL

901 TGGTTCAGATCATCAAGTCCCAGATGATGTGTGCGGAGGACACCC
euValGlnIleIleLysSerGlnMetMetCysAlaGluAspThrH

946 ACAGGGAGAAGTTCTGCTATGAGCTAACTGGAGAGCCCTTGGTCT
isArgGluLysPheCysTyrGluLeuThrGlyGluProLeuValC

991 GCTCCATGGAGGGCACGTGGTACCTGGTGGGATTGGTGAGCTGGG
ysSerMetGluGlyThrTrpTyrLeuValGlyLeuValSerTrpG

1036 GTGCAGGCTGCCAGAAGAGCGAGGCCCCACCCATCTACCTACAGG
lyAlaGlyCysGlnLysSerGluAlaProProIleTyrLeuGlnV

1081 TCTCCTCCTACCAACACTGGATCTGGGACTGCCTCAACGGGCAGG
alSerSerTyrGlnHisTrpIleTrpAspCysLeuAsnGlyGlnA

1126 CCCTGGCCCTGCCAGCCCCATCCAGGACCCTGCTCCTGGCACTCC
laLeuAlaLeuProAlaProSerArgThrLeuLeuLeuAlaLeuP

1171 CACTGCCCCTCAGCCTCCTTGCTGCCCTCTGACTCTGTGTGCCCT
roLeuProLeuSerLeuLeuAlaAlaLeu

1216 CCCTCACTTGTGGGCCCCCCTTGCCTCCGTGCCCAGGTTGCTGTG
1261 GGTGCAGCTGTCACAGCCCTGAGAGTCAGGGTGGAGATGAGGTGC
1306 TCAATTAAACATTACTGTTTTCCATGTAAAAAAAAAAAAAAAAAA
1351 AAAAAAAAA

Fig. 7 (continued)

CACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCCCCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACC
81
AGTGATGGTAAGTGCTGGCCCAGACTGAAGCTCGGAGAGGCACTCTGCTTGCCCAGCGTCACAGTCTTAGCTCCCAACTG
161
TCCTGGCTTCCAGTCTCCCTTGCTTCCCAGATCCCAGACTCTAGCCCCAGCCCCGTCTCTTTCACCAGCTCCTGGGACCC
241
TACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAACTGTATCTACAACCAGCTGCACCAGCGACACCTGTCC
321
AACCCGGCCCGGCCTGGGATGCTATGTGGGGGCCCCCAGCCTGGGGTGCAGGGCCCCTGTCAGGTCTGATAGGGAGAAGA
401
GAAGGAGCAGAAGGGGAGGGGCCTAACCCTGGGCTGGGGGTTGGACTCACAGGACTGGGGGAAAGAGCTGCAATCAGAGG
481
GTGTCTGCCATAGCTGGGCTCAGGCATCTGTCCTTGGCTTTGTTGCCTGGCTCCAGGGAGATTCCGGGGGCCCTGTGCTG
561
TGCCTCGAGCCTGACGGACACTGGGTTCAGGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGT
641
GCTGCTGACCAACACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTTTCCTGGCCCAGAGCCCAG
721
AGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCC
     MetSerAspGluAspSerCysValAlaCysGlySerLeuArgThrAlaGlyProGlnAlaGlyAlaPro
801
TCCCCATGGCCCTGGGAGGCCAGGCTGATGCACCAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTCAGAGGAGGCGGT
SerProTrpProTrpGluAlaArgLeuMetHisGlnGlyGlnLeuAlaCysGlyGlyAlaLeuValSerGluGluAlaVa
881
GCTAACTGCTGCCCACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCGGAGGAGT
lLeuThrAlaAlaHisCysPheIleGlyArgGlnAlaProGluGluTrpSerValGlyLeuGlyThrArgProGluGluT
961
GGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGGCTACGACATGGCCCTCCTGCTGCTGGCC
rpGlyLeuLysGlnLeuIleLeuHisGlyAlaTyrThrHisProGluGlyGlyTyrAspMetAlaLeuLeuLeuLeuAla
1041
CAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCCTCTGCCTGCCCTATGCTGACCACCACCTGCCTGATGGGGAGCGTGG
GlnProValThrLeuGlyAlaSerLeuArgProLeuCysLeuProTyrAlaAspHisHisLeuProAspGlyGluArgGl
1121
CTGGGTTCTGGGACGGGCCCGCCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGGCCTAGGG
yTrpValLeuGlyArgAlaArgProGlyAlaGlyIleSerSerLeuGlnThrValProValThrLeuLeuGlyProArgA
1201
CCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGGTGTGTACCAGTGCTGTGGGT
laCysSerArgLeuHisAlaAlaProGlyGlyAspGlySerProIleLeuProGlyMetValCysThrSerAlaValGly
1281
GAGCTGCCCAGCTGTGAGGTGAGCCCCAGGCCCCCACACCTTACCTAACAGGCCCCTGGCATCCCCTCACCCAATAGCTC
GluLeuProSerCysGluValSerProArgProProHisLeuThr
1361
AAGAACGGACCTTCCAGGCTTGGCCTCTGGACCCACCTCCCACCTGAAGCTAAGCCTTTTTGCCAATTAGCCCCCAAACA
1441
GCCAG

Fig. 8

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  1   CTTAACAGCCACTTGTTTCATCCCACCTGGGCATTAGGTTGACTT

 46   CAAAGATGCCTCAGTTACTGCAAAACATTAATGGGATCATCGAGG
           MetProGlnLeuLeuGlnAsnIleAsnGlyIleIleGluA

 91   CCTTCAGGCGCTATGCAAGGACGGAGGGCAACTGCACAGCGCTCA
      laPheArgArgTyrAlaArgThrGluGlyAsnCysThrAlaLeuT

136   CCCGAGGGGAGCTGAAAAGACTCTTGGAGCAAGAGTTTGCCGATG
      hrArgGlyGluLeuLysArgLeuLeuGluGlnGluPheAlaAspV

181   TGATTGTGAAACCCCACGATCCAGCAACTGTGGATGAGGTCCTGC
      alIleValLysProHisAspProAlaThrValAspGluValLeuA

226   GTCTGCTGGATGAAGACCACACAGGGACTGTGGAATTCAAGGAAT
      rgLeuLeuAspGluAspHisThrGlyThrValGluPheLysGluP

271   TCCTGGTCTTAGTGTTTAAAGTTGCCCAGGCCTGTTTCAAGACAC
      heLeuValLeuValPheLysValAlaGlnAlaCysPheLysThrL

316   TGAGCGAGAGTGCTGAGGGAGCCTGCGGCTCTCAAGAGTCTGGAA
      euSerGluSerAlaGluGlyAlaCysGlySerGlnGluSerGlyS

361   GCCTCCACTCTGGGGCCTCGCAGGAGCTGGGCGAAGGACAGAGAA
      erLeuHisSerGlyAlaSerGlnGluLeuGlyGluGlyGlnArgS

406   GTGGCACTGAAGTGGGAAGGGCGGGGAAAGGGCAGCATTATGAGG
      erGlyThrGluValGlyArgAlaGlyLysGlyGlnHisTyrGluG

451   GGAGCAGCCACAGACAGAGCCAGCAGGGTTCCAGAGGGCAGAACA
      lySerSerHisArgGlnSerGlnGlnGlySerArgGlyGlnAsnA

496   GGCCTGGGGTTCAGACCCAGGGTCAGGCCACTGGCTCTGCGTGGG
      rgProGlyValGlnThrGlnGlyGlnAlaThrGlySerAlaTrpV

541   TCAGCAGCTATGACAGGCAAGCTGAGTCCCAGAGCCAGGAAAGAA
      alSerSerTyrAspArgGlnAlaGluSerGlnSerGlnGluArgI

586   TAAGCCCGCAGATACAACTCTCTGGGCAGACAGAGCAGACCCAGA
      leSerProGlnIleGlnLeuSerGlyGlnThrGluGlnThrGlnL

631   AAGCTGGAGAAGGCAAGAGGAATCAGACAACAGAGATGAGGCCAG
      ysAlaGlyGluGlyLysArgAsnGlnThrThrGluMetArgProG

676   AGAGACAGCCACAGACCAGGGAACAGGACAGAGCCCACCAGACAG
      luArgGlnProGlnThrArgGluGlnAspArgAlaHisGlnThrG
```

Fig. 9

```
721   GTGAGACTGTGACTGGATCTGGAACTCAGACCCAGGCAGGTGCCA
      lyGluThrValThrGlySerGlyThrGlnThrGlnAlaGlyAlaT

766   CCCAGACTGTGGAGCAGGACAGCAGCCACCAGACAGGAAGCACCA
      hrGlnThrValGluGlnAspSerSerHisGlnThrGlySerThrS

811   GCACCCAGACACAGGAGTCCACCAATGGCCAGAACAGAGGGACTG
      erThrGlnThrGlnGluSerThrAsnGlyGlnAsnArgGlyThrG

856   AGATCCACGGTCAAGGCAGGAGCCAGACCAGCCAGGCTGTGACAG
      luIleHisGlyGlnGlyArgSerGlnThrSerGlnAlaValThrG

901   GAGGACACACTCAGATACAGGCAGGGTCACACACCGAGACTGTGG
      lyGlyHisThrGlnIleGlnAlaGlySerHisThrGluThrValG

946   AGCAGGACAGAAGCCAAACTGTAAGCCACGGAGGGGCTAGAGAAC
      luGlnAspArgSerGlnThrValSerHisGlyGlyAlaArgGluG

991   AGGGACAGACCCAGACGCAGCCAGGCAGTGGTCAAAGATGGATGC
      lnGlyGlnThrGlnThrGlnProGlySerGlyGlnArgTrpMetG

1036  AAGTGAGCAACCCTGAGGCAGGAGAGACAGTACCGGGAGGACAGG
      lnValSerAsnProGluAlaGlyGluThrValProGlyGlyGlnA

1081  CCCAGACTGGGGCAAGCACTGAGTCAGGAAGGCAGGAGTGGAGCA
      laGlnThrGlyAlaSerThrGluSerGlyArgGlnGluTrpSerS

1126  GCACTCACCCAAGGCGCTGTGTGACAGAAGGGCAGGGAGACAGAC
      erThrHisProArgArgCysValThrGluGlyGlnGlyAspArgG

1171  AGCCCACAGTGGTTGGTGAGGAATGGGTTGATGACCACTCAAGGG
      lnProThrValValGlyGluGluTrpValAspAspHisSerArgG

1216  AGACAGTGATCCTCAGGCTGGACCAGGGCAACTTGCATACCAGTG
      luThrValIleLeuArgLeuAspGlnGlyAsnLeuHisThrSerV

1261  TTTCCTCAGCACAGGGCCAGGATGCAGCCCAGTCAGAAGAGAAGC
      alSerSerAlaGlnGlyGlnAspAlaAlaGlnSerGluGluLysA

1306  GAGGCATCACAGCTAGAGAGCTGTATTCCTACTTGAGAAGCACCA
      rgGlyIleThrAlaArgGluLeuTyrSerTyrLeuArgSerThrL

1351  AGCCATGACTTCCCCGACTCCAATGTCCAGTACTGGAAGAAGACA
      ysPro

1396  GCTGGAGAGAGTTTGGCTTGTCCTGCATGGCCAATCCAGTGGGTG
1441  CATCCCTGGACATCAGCTCTTCATTATGCAGCTTCCCTTTTAGGT
1486  CTTTCTCAATGAGATAATTTCTGCAAGGAGCTTTCTATCCTGAAC
1531  TCTTCTTTCTTACCTGCTTTGCGGTGCAGACCCTCTCAGGAGCAG
1576  GAAGACTCAGAACAAGTCACCCCTT
```

Fig. 9 (continued)

1. 11618130.0.184_Cura_108
2. 11618130.0.27_Cura_56

```
1161813300184_cura_108   MSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFHGR
11618130027_cura_56      MSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFNGR

1161813300184_cura_108   QAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYA
11618130027_cura_56      QAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRALCLPYF

1161813300184_cura_108   DHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTS
11618130027_cura_56      DHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTS

1161813300184_cura_108   AVGELPSCEVSPRPPHET------------------------------
11618130027_cura_56      AVGELPSCEGLSGAPIVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVSSLDW

1161813300184_cura_108   ------------------------
11618130027_cura_56      QVYFAEEPEPEAEPGSCLANISQPTSC
```

Fig. 10

Sequences analyzed:

1. 14578444-0-47_Cura_56
2. 14578444-0-143Cura_56

```
14578444047_cura_56    MEKMLAGCFLLILGQIVLLPCEARERSRGRSISRGRHARTHPQTALLESSCENKRADLVF
145784440143_cura_56   MEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGRHARTHPQTALLESSCENKRADLVF

14578444047_cura_56    IIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEV
145784440143_cura_56   IIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEV

14578444047_cura_56    ERAVKRMRHLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEV
145784440143_cura_56   ERAVKRMRHLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEV

14578444047_cura_56    AAKARDTGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAH
145784440143_cura_56   AAKARDTGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAH

14578444047_cura_56    MCSTLEHNCAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGS
145784440143_cura_56   MCSTLEHNCAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGS

14578444047_cura_56    FVCECYSGYALAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCT
145784440143_cura_56   FVCECYSGYALAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCT
```

Fig. 11

```
14578444047_cura_56    KIDYCASSNHGCQYECVNTDDSYSCHCLKGFTLNPDKKTCRRINYCALNKPGCEHECVNM
145784440143_cura_56   KIDYCASSNHGCQYECVNTDDSYSCHCLKGFTLNPDKKTCRRINYCALNKPGCEHECVNM

14578444047_cura_56    EESYYCRCHRGYTLDPNGKPCSRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLINEDLK
145784440143_cura_56   EESYYCRCHRGYTLDPNGKPCSRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLINEDLK

14578444047_cura_56    TCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTCAKLDSCALGDHGCEHSC
145784440143_cura_56   TCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTCAKLDSCALGDHGCEHSC

14578444047_cura_56    VSSEDSFVCQCFEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLTE
145784440143_cura_56   VSSEDSFVCQCFEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLTE

14578444047_cura_56    DGKRCRISSGKDVCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLV
145784440143_cura_56   DGKRCRISSGKDVCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLV

14578444047_cura_56    FVIDGSKSLGEENFEVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKD
145784440143_cura_56   FVIDGSKSLGEENFEVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKD

14578444047_cura_56    MKKAVAHMKYMGKGSMTGLALKHMFERSFTQGEGARPFSTRVPRAAIVFTDGRAQDDVSE
145784440143_cura_56   MKKAVAHMKYMGKGSMTGLALKHMFERSFTQGEGARPLFHKGAQSSHCVHRRTGSG~~~~

14578444047_cura_56    WASKAKANGITMYAVGVGKAIEEELQEIASEPTNKHLFYAEDFSTMDEISEKLKKGICEA
145784440143_cura_56   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

14578444047_cura_56    LEDSDGRQDSPAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQK
145784440143_cura_56   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

14578444047_cura_56    LSHSTKPSGSPLEEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR
145784440143_cura_56   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
```

Fig. 11 (continued)

98 —
64 —
50 —
36 —
30 —
16 —
6 —

Fig. 12

98 —
64 —
50 —
36 —
30 —
16 —
6 —
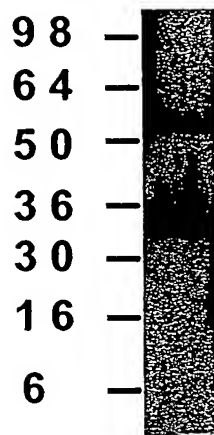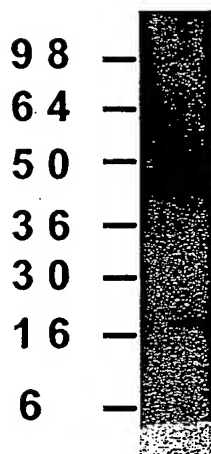
Fig. 13

Normal & Tumor Tissues	11696905	16406477.0.206	214433858	216372620.64
Endothelial cells	3.5	0.0	6.6	0.0
Endothelial cells (treated)	2.9	0.0	2.0	0.0
Pancreas	9.4	3.1	1.2	0.0
Pancreatic ca. CAPAN 2	3.7	0.0	0.3	0.0
Adipose	60.7	0.3	22.5	0.8
Adrenal gland	18.0	0.0	3.2	0.2
Thyroid	13.8	0.0	4.6	2.4
Salivary gland	0.0	0.6	0.7	36.3
Pituitary gland	2.2	0.6	4.0	1.4
Brain (fetal)	3.1	0.5	6.9	0.7
Brain (whole)	4.4	0.7	24.5	0.3
Brain (amygdala)	17.2	0.1	5.0	0.4
Brain (cerebellum)	1.6	1.2	41.8	1.4
Brain (hippocampus)	9.3	0.8	10.4	0.6
Brain (hypothalamus)	5.7	10.0	2.3	0.5
Brain (substantia nigra)	33.2	0.7	5.2	0.1
Brain (thalamus)	22.7	0.5	5.2	0.0
Spinal cord	21.8	0.3	4.0	1.5
CNS ca. (glio/astro) U87-MG	2.2	0.0	1.0	0.0
CNS ca. (glio/astro) U-118-MG	4.5	0.0	1.5	0.0
CNS ca. (astro) SW1783	0.0	0.0	0.7	0.0
CNS ca.* (neuro; met) SK-N-AS	2.7	0.0	12.6	0.1
CNS ca. (astro) SF-539	0.2	0.0	0.0	0.0
CNS ca. (astro) SNB-75	1.3	0.0	0.6	0.0
CNS ca. (glio) SNB-19	0.6	0.0	0.8	0.2
CNS ca. (glio) U251	0.2	0.0	3.6	0.1
CNS ca. (glio) SF-295	6.2	0.1	0.2	0.0
Heart	10.7	0.1	1.3	0.1
Skeletal muscle	18.4	0.0	0.2	0.2
Bone marrow	11.1	0.0	0.1	0.0
Thymus	7.3	0.9	2.5	0.5
Spleen	2.9	0.1	1.4	0.0
Lymph node	4.3	0.1	1.3	0.1

Fig. 14

Normal & Tumor Tissues	11696905	16406477.0.206	214433858	216637262.0.64
Colon (ascending)	1.3	0.2	5.1	1.3
Stomach	5.4	0.2	5.7	0.0
Small intestine	7.0	0.2	1.7	0.0
Colon ca. SW480	0.4	0.0	0.0	0.1
Colon ca.* (SW480 met)SW620	0.1	0.0	0.0	0.0
Colon ca. HT29	0.4	0.0	0.0	0.1
Colon ca. HCT-116	4.4	0.0	0.0	0.0
Colon ca. CaCo-2	1.1	0.1	0.1	0.0
Colon ca. HCT-15	11.0	0.2	0.3	0.2
Colon ca. HCC-2998	0.0	0.0	1.3	0.0
Gastric ca.* (liver met) NCI-N87	4.9	0.3	1.9	0.0
Bladder	18.8	0.1	10.8	0.1
Trachea	4.8	0.0	2.2	100.0
Kidney	7.3	0.4	13.1	0.1
Kidney (fetal)	11.0	1.8	29.5	0.1
Renal ca. 786-0	0.4	0.0	0.0	0.0
Renal ca. A498	56.3	0.0	0.0	0.1
Renal ca. RXF 393	2.7	0.0	0.1	0.0
Renal ca. ACHN	1.0	0.0	0.1	0.1
Renal ca. UO-31	1.8	0.0	0.4	0.1
Renal ca. TK-10	13.4	0.5	0.2	0.1
Liver	74.7	0.7	2.1	0.1
Liver (fetal)	27.7	1.2	0.9	0.0
Liver ca. (hepatoblast HepG2	7.4	0.0	0.0	0.0
Lung	9.9	0.0	2.9	0.0
Lung (fetal)	1.5	1.5	3.0	0.0
Lung ca. (small cell) LX-1	0.4	0.0	0.0	0.0
Lung ca. (small cell) NCI-H69	0.5	0.1	9.3	0.5
Lung ca. (s.cell var.) SHP-77	0.6	0.4	100.0	1.7
Lung ca. (large cell) NCI-H460	20.6	0.3	66.9	0.6
Lung ca. (non-sm. cell) A549	3.3	0.0	15.5	0.1
Lung ca. (non-s.cell) NCI-H23	7.4	0.5	9.0	0.0
Lung ca (non-s.cell) HOP-62	32.1	0.1	1.5	0.1
Lung ca. (non-s.cl) NCI-H522	11.0	0.6	0.0	0.0
Lung ca. (squam.) SW 900	3.3	0.9	6.1	0.1

Fig. 14 (continued)

Normal & Tumor Tissues	11696905.0	16406477.0.206	214433858.0	216637262.0.64
Mammary gland	30.4	1.5	12.2	0.0
Breast ca.* (pl. effusion) MCF-7	4.8	0.0	0.0	0.0
Breast ca.* (pl.ef) MDA-MB-231	2.2	0.0	0.0	0.1
Breast ca.* (pl. effusion) T47D	9.8	0.1	0.9	0.6
Breast ca. BT-549	9.2	0.1	1.2	0.3
Breast ca. MDA-N	1.3	0.0	0.0	0.0
Ovary	6.0	0.3	9.7	0.0
Ovarian ca. OVCAR-3	1.6	0.1	0.8	0.1
Ovarian ca. OVCAR-4	1.9	0.0	0.0	0.0
Ovarian ca. OVCAR-5	7.1	0.3	6.9	0.6
Ovarian ca. OVCAR-8	1.3	2.7	2.7	0.0
Ovarian ca. IGROV-1	0.7	0.2	5.0	0.0
Ovarian ca.* (ascites) SK-OV-3	2.5	0.0	0.2	0.0
Myometrium	2.3	0.0	41.2	1.2
Uterus	6.3	0.6	25.7	0.1
Placenta	100.0	0.0	94.0	0.1
Prostate	13.3	0.1	3.4	0.1
Prostate ca.* (bone met) PC-3	7.9	1.7	0.2	0.2
Testis	14.3	100.0	37.1	4.0
Melanoma Hs688(A).T	1.4	0.0	0.0	0.0
Melanoma* (met) Hs688(B).T	5.3	0.0	0.0	0.0
Melanoma UACC-62	0.6	0.0	0.0	0.0
Melanoma M14	0.9	0.1	0.3	0.2
Melanoma LOX IMVI	1.0	0.0	0.0	0.1
Melanoma* (met) SK-MEL-5	0.0	0.0	8.7	0.0
Melanoma SK-MEL-28	100.0	0.0	0.0	0.0

Fig. 14 (continued)

Figure 15. Nucleotide Sequence for CG106318-01.

```
>CG106318-01 4810 nt
GTCCATGGGGCCGATGTATGGGAGATGAATGTGGTCCCGGAGGCATCCAAACGAGGGCTG
TGTGGTGTGCTCATGTGGAGGGATGGACTACACTGCATACTAACTGTAAGCAGGCCGAGA
GACCCAATAACCAGCAGAATTGTTTCAAAGTTTGCGATTGGCACAAAGAGTTGTACGACT
GGAGACTGGGACCTTGGAATCAGTGTCAGCCCGTGATTTCAAAAAGCCTAGAGAAACCTC
TTGAGTGCATTAAGGGGGAAGAAGGTATTCAGGTGAGGGAGATAGCGTGCATCCAGAAAG
ACAAAGACATTCCTGCGGAGGATATCATCTGTGAGTACTTTGAGCCCAAGCCTCTCCTGG
AGCAGGCTTGCCTCATTCCTTGCCAGCAAGATTGCATCGTGTCTGAATTTTCTGCCTGGT
CCGAATGCTCCAAGACCTGCGGCAGCGGGCTCCAGCACCGGACGCGTCATGTGGTGGCGC
CCCCGCAGTTCGGAGGCTCTGGCTGTCCAAACCTGACGGAGTTCCAGGTGTGCCAATCCA
GTCCATGCGAGGCCGAGGAGCTCAGGTACAGCCTGCATGTGGGGCCCTGGAGCACCTGCT
CAATGCCCCACTCCCGACAAGTAAGACAAGCAAGGAGACGCGGGAAGAATAAAGAACGGG
AAAAGGACCGCAGCAAAGGAGTAAAGGATCCAGAAGCCCGCGAGCTTATTAAGAAAAAGA
GAAACAGAAACAGGCAGAACAGACAAGAGAACAAATATTGGGACATCCAGATTGGATATC
AGACCAGAGAGGTTATGTGCATTAACAAGACGGGGAAAGCTGCTGATTTAAGCTTTTGCC
AGCAAGAGAAGCTTCCAATGACCTTCCAGTCCTGTGTGATCACCAAAGAGTGCCAGGTTT
CCGAGTGGTCAGAGTGGAGCCCCTGCTCAAAAACATGCCATGACATGGTGTCCCCTGCAG
GCACTCGTGTAAGGACACGAACCATCAGGCAGTTTCCCATTGGCAGTGAAAAGGAGTGTC
CAGAATTTGAAGAAAAAGAACCCTGTTTGTCTCAAGGAGATGGAGTTGTCCCCTGTGCCA
CGTATGGCTGGAGAACTACAGAGTGGACTGAGTGCCGTGTGGACCCTTTGCTCAGTCAGC
AGGACAAGAGGCGCGGCAACCAGACGGCCCTCTGTGGAGGGGGCATCCAGACCCGAGAGG
TGTACTGCGTGCAGGCCAACGAAAACCTCCTCTCACAATTAAGTACCCACAAGAACAAAG
AAGCCTCAAAGCCAATGGACTTAAAATTATGCACTGGACCTATCCCTAATACTACACAGC
TGTGCCACATTCCTTGTCCAACTGAATGTGAAGTTTCACCTTGGTCAGCTTGGGGACCTT
GTACTTATGAAAACTGTAATGATCAGCAAGGGAAAAAAGGCTTCAAACTGAGGAAGCCGGC
GCATTACCAATGAGCCCACTGGAGGCTCTGGGGTAACCGGAAACTGCCCTCACTTACTGG
AAGCCATTCCCTGTGAAGAGCCTGCCTGTTATGACTGGAAAGCGGTGAGACTGGGAGACT
GCGAGCCAGATAACGGAAAGGAGTGTGGTCCAGGCACGCAAGTTCAAGAGGTTGTGTGCA
TCAACAGTGATGGAGAAGAAGTTGACAGACAGCTGTGCAGAGATGCCATCTTCCCCATCC
CTGTGGCCTGTGATGCCCCATGCCCGAAAGACTGTGTGCTCAGCACATGGTCTACGTGGT
CCTCCTGCTCACACACCTGCTCAGGGAAAACGACAGAAGGGAAACAGATACGAGCACGAT
CCATTCTGGCCTATGCGGGTGAAGAAGGTGGAATTCGCTGTCCAAATAGCAGTGCTTTGC
AAGAAGTACGAAGCTGTAATGAGCATCCTTGCACAGTGTACCACTGGCAAACTGGTCCCT
GGGGCCAGTGCATTGAGGACACCTCAGTATCGTCCTTCAACACAACTACGACTTGGAATG
GGGAGGCCTCCTGCTCTGTCGGCATGCAGACAAGAAAAGTCATCTGTGTGCGAGTCAATG
TGGGCCAAGTGGGACCCAAAAAATGTCCTGAAAGCCTTCGACCTGAAACTGTAAGGCCTT
GTCTGCTTCCTTGTAAGAAGGACTGTATTGTGACCCCATATAGTGACTGGACATCATGCC
CCTCTTCGTGTAAAGAAGGGGACTCCAGTATCAGGAAGCAGTCTAGGCATCGGGTCATCA
TTCAGCTGCCAGCCAACGGGGGCCGAGACTGCACAGATCCCCTCTATGAAGAGAAGGCCT
GTGAGGCACCTCAAGCGTGCCAAAGCTACAGGTGGAAGACTCACAAATGGCGCAGATGCC
AATTAGTCCCTTGGAGCGTGCAACAAGACAGCCCTGGAGCACAGGAAGGCTGTGGGCCTG
GGCGACAGGCAAGAGCCATTACTTGTCGCAAGCAAGATGGAGGACAGGCTGGAATCCATG
AGTGCCTACAGTATGCAGGCCCTGTGCCAGCCCTTACCCAGGCCTGCCAGATCCCCTGCC
AGGATGACTGTCAATTGACCAGCTGGTCCAAGTTTTCTTCATGCAATGGAGACTGTGGTG
CAGTTAGGACCAGAAAGCGCACTCTTGTTGGAAAAAGTAAAAGAAGGAAAAATGTAAAA
ATTCCCATTTGTATCCCCTGATTGAGACTCAGTATTGTCCTTGTGACAAATATAATGCAC
AACCTGTGGGGAACTGGTCAGACTGTATTTTTACCAGAGGGAAAAGTGGAAGTGTTGCTGG
GAATGAAAGTACAAGGAGACATCAAGGAATGCGGACAAGGATATCGTTACCAAGCAATGG
CATGCTACGATCAAAATGGCAGGCTTGTGGAAACATCTAGATGTAACAGCCATGGTTACA
TTGAGGAGGCCTGCATCATCCCCTGCCCCTCAGACTGCAAGCTCAGTGAGTGGTCCAACT
GGTCGCGCTGCAGCAAGTCCTGTGGGAGTGGTGTGAAGGTTCGTTCTAAATGGCTGCGTG
AAAAACCATATAATGGAGGAAGGCCTTGCCCCAAACTGGACCATGTCAACCAGGCACAGG
TGTATGAGGTTGTCCCATGCCACAGTGACTGCAACCAGTACCTATGGGTCACAGAGCCCT
GGAGCATCTGCAAGGTGACCTTTGTGAATATGCGGGAGAACTGTGGAGAGGGCGTGCAAA
CCCGAAAAGTGAGATGCATGCAGAATACAGCAGATGGCCCTTCTGAACATGTAGAGGATT
ACCTCTGTGACCCAGAAGAGATGCCCCTGGGCTCTAGAGTGTGCAAATTACCATGCCCTG
AGGACTGTGTGATATCTGAATGGGGTCCATGGACCCAATGTGTTTTGCCTTGCAATCAAA
GCAGTTTCCGGCAAAGGTCAGCTGATCCCATCAGACAACCAGCTGATGAAGGAAGATCTT
GCCCTAATGCTGTTGAGAAAGAACCCTGTAACCTGAACAAAAACTGCTACCACTATGATT
ATAATGTAACAGACTGGAGTACATGTCAGCTGAGTGAGAAGGCAGTTTGTGGAAATGGAA
TAAAAACAAGGATGTTGGATTGTGTTCGAAGTGATGGCAAGTCAGTTGACCTGAAATATT
```

GTGAAGCGCTTGGCTTGGAGAAGAACTGGCAGATGAACACGTCCTGCATGGTGGAATGCC
CTGTGAACTGTCAGCTTTCTGATTGGTCTCCTTGGTCAGAATGTTCTCAAACATGTGGCC
TCACAGGAAAAATGATCCGAAGACGAACAGTGACCCAGCCCTTTCAAGGTGATGGAAGAC
CATGCCCTTCCCTGATGGACCAGTCCAAACCCTGCCCAGTGAAGCCTTGTTATCGGTGGC
AATATGGCCAGTGGTCTCCATGCCAAGTGCAGGAGCCCAGTGTGGAGAAGGGACCAGAA
CAAGGAACATTTCTTGTGTAGTAAGTGATGGGTCAGCTGATGATTTCAGCAAAGTGGTGG
ATGAGGAATTCTGTGCTGACATTGAACTCATTATAGATGGTAATAAAAATATGGTTCTGG
AGGAATCCTGCAGCCAGCCTTGCCCAGGTGACTGTTATTTGAAGGACTGGTCTTCCTGGA
GCCTGTGTCAGCTGACCTGTGTGAATGGTGAGGATCTAGGCTTTGGTGGAATACAGGTCA
GATCCAGACCGGTGATTATACAAGAACTAGAGAATCAGCATCTGTGCCCAGAGCAGATGT
TAGAAACAAAATCATGTTATGATGGACAGTGCTATGAATATAAATGGATGGCCAGTGCTT
GGAAGGGCTCTTCCCGAACAGTGTGGTGTCAAAGGTCAGATGGTATAAATGTAACAGGGG
GCTGCTTGGTGATGAGCCAGCCTGATGCCGACAGGTCTTGTAACCCACCGTGTAGTCAAC
CCCACTCGTACTGTAGCGAGACAAAAACATGCCATTGTGAAGAAGGGTACACTGAAGTCA
TGTCTTCTAACAGCACCCTTGAGCAATGCACACTTATCCCCGTGGTGGTATTACCCACCA
TGGAGGACAAAAGAGGAGATGTGAAAACCAGTCGGGCTGTACATCCAACCCAACCCTCCA
GTAAACCCAGCAGGACGGGGAAGGACCTGGTTTCTACAGCCATTTGGGCCAGATGGGAGAC
TAAAGACCTGGGTTTACGGTGTAGCAGCTGGGGCATTTGTGTTACTCATCTTTATTGTCT
CCATGATTTATCTAGCTTGCAAAAAGCCAAAGAAACCCCAAAGAAGGCAAAACAACCGAC
TGAAACCTTTAACCTTAGCCTATGATGGAGATGCCGACATGTAACATATAACTTTTCCTG
GCAACAACCA (SEQ ID NO: 40)

Protein Sequence for CG106318-01   ORF Start: 18 ORF Stop: 4782 Frame: 3

Protein Sequence:

>CG106318-01-prot   1588 aa
MGDECGPGGIQTRAVWCAHVEGWTTLHTNCKQAERPNNQQNCFKVCDWHKELYDWRLGPW
NQCQPVISKSLEKPLECIKGEEGIQVREIACIQKDKDIPAEDIICEYFEPKPLLEQACLI
PCQQDCIVSEFSAWSECSKTCGSGLQHRTRHVVAPPQFGGSGCPNLTEFQVCQSSPCEAE
ELRYSLHVGPWSTCSMPHSRQVRQARRRGKNKEREKDRSKGVKDPEARELIKKKRNRNRQ
NRQENKYWDIQIGYQTREVMCINKTGKAADLSFCQQEKLPMTFQSCVITKECQVSEWSEW
SPCSKTCHDMVSPAGTRVRTRTIRQFPIGSEKECPEFEEKEPCLSQGDGVVPCATYGWRT
TEWTECRVDPLLSQQDKRRGNQTALCGGGIQTREVYCVQANENLLSQLSTHKNKEASKPM
DLKLCTGPIPNTTQLCHIPCPTECEVSPWSAWGPCTYENCNDQQGKKGFKLRKRRITNEP
TGGSGVTGNCPHLLEAIPCEEPACYDWKAVRLGDCEPDNGKECGPGTQVQEVVCINSDGE
EVDRQLCRDAIFPIPVACDAPCPKDCVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYA
GEEGGIRCPNSSALQEVRSCNEHPCTVYHWQTGPWGQCIEDTSVSSFNTTTTWNGEASCS
VGMQTRKVICVRVNVGQVGPKKCPESLRPETVRPCLLPCKKDCIVTPYSDWTSCPSSCKE
GDSSIRKQSRHRVIIQLPANGGRDCTDPLYEEKACEAPQACQSYRWKTHKWRRCQLVPWS
VQQDSPGAQEGCGPGRQARAITCRKQDGGQAGIHECLQYAGPVPALTQACQIPCQDDCQL
TSWSKFSSCNGDCGAVRTRKRTLVGKSKKKEKCKNSHLYPLIETQYCPCDKYNAQPVGNW
SDCILPEGKVEVLLGMKVQGDIKECGQGYRYQAMACYDQNGRLVETSRCNSHGYIEEACI
IPCPSDCKLSEWSNWSRCSKSCGSGVKVRSKWLREKPYNGGRPCPKLDHVNQAQVYEVVP
CHSDCNQYLWVTEPWSICKVTFVNMRENCGEGVQTRKVRCMQNTADGPSEHVEDYLCDPE
EMPLGSRVCKLPCPEDCVISEWGPWTQCVLPCNQSSFRQRSADPIRQPADEGRSCPNAVE
KEPCNLNKNCYHYDYNVTDWSTCQLSEKAVCGNGIKTRMLDCVRSDGKSVDLKYCEALGL
EKNWQMNTSCMVECPVNCQLSDWSPWSECSQTCGLTGKMIRRRTVTQPFQGDGRPCPSLM
DQSKPCPVKPCYRWQYGQWSPCQVQEAQCGEGTRTRNISCVVSDGSADDFSKVVDEEFCA
DIELIIDGNKNMVLEESCSQPCPGDCYLKDWSSWSLCQLTCVNGEDLGFGGIQVRSRPVI
IQELENQHLCPEQMLETKSCYDGQCYEYKWMASAWKGSSRTVWCQRSDGINVTGGCLVMS
QPDADRSCNPPCSQPHSYCSETKTCHCEEGYTEVMSSNSTLEQCTLIPVVVLPTMEDKRG
DVKTSRAVHPTQPSSNPAGRGRTWFLQPFGPDGRLKTWVYGVAAGAFVLLIFIVSMIYLA
CKKPKKPQRRQNNRLKPLTLAYDGDADM (SEQ ID NO: 41)

Figure 16. Nucleotide and Protein Sequences for CG50817-04.

>CG50817-04 1447 nt

GCGGACACCAGTGATGCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTCGC
CCCACATGTAACTGTATCTACAACCAGCTGCACCAGCGACACCTGTCCAACCCGGCCCGG
CCTGGGATGCTATGTGGGGGCCCCCAGCCTGGGGTGCAGGGCCCCTGTCAGGTCTGATAG
GGAGAAGAGAAGGAGCAGAAGGGGAGGGGCCTAACCCTGGGCTGGGGGTTGGACTCACAG
GACTGGGGGAAAGAGCTGCAATCAGAGGGTGTCTGCCATAGCTGGGCTCAGGCATCTGTC
CTTGGCTTTGTTGCCTGGCTCCAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCT
GACGGACACTGGGTTCAGGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGAC
GCTCCTGTGCTGCTGACCAACACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAG
GGGGCAGCTTTCCTGGCCCAGAGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGT
GTAGCCTGTGGATCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCCTCCCCATGGCCC
TGGGAGGCCAGGCTGATGCACCAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTCAGAG
GAGGCGGTGCTAACTGCTGCCCACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGC
GTAGGGCTGGGGACCAGACCGGAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCC
TACACCCACCCTGAGGGGGGCTACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACA
CTGGGAGCCAGCCTGCGGCCCCTCTGCCTGCCCTATGCTGACCACCACCTGCCTGATGGG
GAGCGTGGCTGGGTTCTGGGACGGGCCCGCCCAGGAGCAGGCATCAGCTCCCTCCAGACA
GTGCCCGTGACCCTCCTGGGGCCTAGGGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGT
GATGGCAGCCCTATTCTGCCGGGGGATGGTGTGTACCAGTGCTGTGGGTGAGCTGCCCAGC
TGTGAGGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTCTCAGGAACAAGAGAAT
GCAGGCAGGCAAATGGCATTACTGCCCCTGTCCTCCCCACCCTGTCATGTGTGATTCCAG
GCACCAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCTGCCTGGGGCCACAGG
TGCCCACTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCCCACACCCAACTCTGC
TACCAAGCAGGCGTCTCAGCTTTCCTCCTCCTTTACCCTTTCAGATACAATCACGCCAGC
CACGTTGTTTTGAAAATTTCTTTTTTTTGGGGGGGCAGCAGTTTTCCTTTTTTTTAAACTTAA
ATAAATT (SEQ ID NO:42)

Protein Sequence for CG50817-04 ORF Start: 520 ORF Stop: 1192 Frame: 1

Protein Sequence:

>CG50817-04-prot 224 aa

MSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGR
QAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYA
DHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTS
AVGELPSCEANQPAADRGPGHSQEQENAGRQMALLPLSSPPCHV (SEQ ID NO:43)

Figure 17. Nucleotide and Protein Sequences for CG50817-05.

. Nucleotide sequence encoding the Peptidase-like protein of the invention.

```
>CG50817-05
CGCTGGGCCTCTGTCCTGATGCTGCTGAGCTCCCTGGTGTCTCTCGCTGGTTCTGTCTAC    60
CTGGCCTGGATCCTGTTCTTCGTGCTCTATGATTTCTGCATTGTTTGTATCACCACCTAT   120
GCTATCAACGTGAGCCTGATGTGGCTCAGTTTCCGGAAGGTCCAAGAACCCCAGGGCCAA   180
CCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCCTGGCAGGCCAGTGTGAGG   240
AGGCAAGGAGCCCACATCTGCAGCGGCTCCCTGGTGGCAGACACCTGGGTCCTCACTGCT   300
GCCCACTGCTTTGAAAAGGCAGCAGCAACAGAACTGAATTCCTGCGTGAGGGACTCAGCC   360
CCTGGGGCCGAAGAGGTGGGGGTGGCTGCCCTGCAGTTGCCCAGGGCCTATAACCACTAC   420
AGCCAGGGCTCAGACCTGGCCCTGCTGCAGCTCGCCCACCCCACGACCCACACACCCCTC   480
TGCCTGCCCCAGCCCGCCCATCGCTTCCCCTTTGGAGCCTCCTGCTGGGCCACTGGCTGG   540
GATCAGGACACCAGTGATGCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGT   600
CGCCCCACATGTAACTGTATCTACAACCAGCTGCACCAGCGACACCTGTCCAACCCGGCC   660
CGGCCTGGGATGCTATGTGGGGGCCCCCAGCCTGGGGTGCAGGGCCCCTGTCAGGGAGAT   720
TCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGGTTCAGGCTGGCATCATC   780
AGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGTGCTGCTGACCAACACAGCTGCT   840
CACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTTTCCTGGCCCAGAGCCCAGAG   900
ACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGGACAGCAGGT   960
CCCCAGGCAGGAGCACCCTCCCCATGGCCCTGGGAGGCCAGGCTGATGCACCAGGGACAG  1020
CTGGCCTGTGGCGGAGCCCTGGTGTCAGAGGAGGCGGTGCTAACTGCTGCCCACTGCTTC  1080
ATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCGGAGGAGTGG  1140
GGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGGCTACGACATG  1200
GCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCCTCTGCCTG  1260
CCCTATGCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCTGGGACGGGCCCGC  1320
CCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGGCCTAGGGCC  1380
TGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGGTG  1440
TGTACCAGTGCTGTGGGTGAGCTGCCCAGCTGTGAGGCCAACCAACCAGCTGCTGACAGG  1500
GGACCTGGCCATTCTCAGGAACAAGAGAATGCAGGCAGGCAAATGGCATTACTGCCCCTG  1560
TCCTCCCCACCCTGTCATGTGTGATTCCAGGC                               1592
(SEQ ID NO:44)
```

Protein sequence encoded by the coding sequence shown above.

```
>CG50817-05
MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGQPKPQEG    60
NTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSCVRDSAPGAEEV   120
GVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATGWDQDTSD   180
APGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVL   240
CLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSPETPEMSD   300
EDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAP   360
EEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYADHH   420
LPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTSAVG   480
ELPSCEANQPAADRGPGHSQEQENAGRQMALLPLSSPPCHV                      521
      (SEQ ID NO:45)
```

Figure 18. Nucleotide and Protein Sequences for CG50817-06.

Nucleotide sequence encoding the Peptidase-like protein of the invention.

```
>CG50817-06
AGCGACACCTGTCCAACCCGGCCCGGCCTGGGATGCTATGTGGGGGCCCCCAGCCTGGGG    60
TGCAGGGCCCCTGTCAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGAC   120
ACTGGGTTCAGGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTG   180
TGCTGCTGACCAACACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCAG   240
CTTTCCTGGCCCAGAGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCT   300
GTGGATCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCCTCCCCATGGCCCTGGGAGG   360
CCAGGCTGATGCACCAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTCAGAGGAGGCGG   420
TGCTAACTGCTGCCCACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGC   480
TGGGGACCAGACCGGAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCC   540
ACCCTGAGGGGGGCTACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAG   600
CCAGCCTGCGGCCCCTCTGCCTGCCCTATGCTGACCACCACCTGCCTGATGGGGAGCGTG   660
GCTGGGTTCTGGGACGGGCCCGCCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCG   720
TGACCCTCCTGGGGCCTAGGGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCA   780
GCCCTATTCTGCCGGGGATGGTGTGTACCAGTGCTGTGGGTGAGCTGCCCAGCTGTGAGG   840
CCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTCTCAGGAACAAGAGAATGCAGGCA   900
GGCAAATGGCATTACTGCCCCTGTCCTCCCCACCCTGTCATGTGTGATTCCAGGCACCAG   960
GGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCTGCCTGGGGCCACAGGTGCCCAC  1020
TCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCCCACACCCAACTCTGCTACCAAG  1080
CAGGCGTCTCAGCTTTCCTCCTCCTTTACCCTTTCAGATACAATCACGCCAGCCACGTTG  1140
TTTTGAAAATTTCTTTTTTTGGGGGGGCAGCAGTTTTCCTTTTTTTTAAACTTAAATAAATT  1200
(SEQ ID NO:46)
```

Protein sequence encoded by the coding sequence shown above.

```
>CG50817-06
MLCGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSS    60
WLQARVQGAAFLAQSPETPEMSDEDSCVACGSLRTAGPQAGAPSPWPWEARLMHQGQLAC   120
GGALVSEEAVLTAAHCFIGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALL   180
LLAQPVTLGASLRPLCLPYADHHLPDGERGWVLGRARPGAGISSLQTVPVTLLGPRACSR   240
LHAAPGGDGSPILPGMVCTSAVGELPSCEANQPAADRGPGHSQEQENAGRQMALLPLSSP   300
PCHV                                                          304
(SEQ ID NO:47)
```

Figure 19. Nucleotide and Protein Sequences For CG51099-03.

Nucleotide sequence encoding the Serine Protease-like protein of the invention.

```
>CG51099-03
CGGAGAGACGCAGTCGGCTGCCACCCCGGGATGGGTCGCTGGTGCCAGACCGTCGCGCGC     60
GGGCAGCGCCCCCGGACGTCTGCCCCCTCCCGCGCCGGTGCCCTGCTGCTGCTGCTTCTG    120
TTGCTGAGGTCTGCAGGTTGCTGGGGCGCAGGGGAAGCCCCGGGGGCGCTGTCCACTGCT    180
GATCCCGCCGACCAGAGCGTCCAGTGTGTCCCCAAGGCCACCTGTCCTTCCAGCCGGCCT    240
CGCCTTCTCTGGCAGACCCCGACCACCCAGACACTGCCCTCGACCACCATGGAGACCCAA    300
TTCCCAGTTTCTGAAGGCAAAGTCGACCCATACCGCTCCTGTGGCTTTTCCTACGAGCAG    360
GACCCCACCCTCAGGGACCCAGAAGCCGTGGCTCGGCGGTGGCCCTGGATGGTCAGCGTG    420
CGGGCCAATGGCACACACATCTGTGCCGGCACCATCATTGCCTCCCAGTGGGTGCTGACT    480
GTGGCCCACTGCCTGATCTGGCGTGATGTTATCTACTCAGTGAGGGTGGGGAGTCCGTGG    540
ATTGACCAGATGACGCAGACCGCCTCCGATGTCCCGGTGCTCCAGGTCATCATGCATAGC    600
AGGTACCGGGCCCAGCGGTTCTGGTCCTGGGTGGCCAGGCCAACGACATCGGCCTCCTC    660
AAGCTCAAGCAGGAACTCAAGTACAGCAATTACGTGCGGCCCATCTGCCTGCCTGGCACG    720
GACTATGTGTTGAAGGACCATTCCCGCTGCACTGTGACGGGCTGGGGACTTTCCAAGGCT    780
GACGGCATGTGGCCTCAGTTCCGGACCATTCAGGAGAAGGAAGTCATCATCCTGAACAAC    840
AAAGAGTGTGACAATTTCTACCACAACTTCACCAAAATCCCCACTCTGGTTCAGATCATC    900
AAGTCCCAGATGATGTGTGCGGAGGACACCCACAGGGAGAAGTTCTGCTATGAGCTAACT    960
GGAGAGCCCTTGGTCTGCTCCATGGAGGGCACGTGGTACCTGGTGGGATTGGTGAGCTGG   1020
GGTGCAGGCTGCCAGAAGAGCGAGGCCCCCACCCATCTACCTACAGGTCTCCTCCTACCAA   1080
CACTGGATCTGGGACTGCCTCAACGGGCAGGCCCTGGCCCTGCCAGCCCCATCCAGGACC   1140
CTGCTCCTGGCACTCCCACTGCCCCTCAGCCTCCTTGCTGCCCTCTGACTCTGTGTGCCC   1200
TCCCTCACTTGTGA                                                 1214
(SEQ ID NO:48)
```

Protein sequence encoded by the nucleotide sequence shown above.

```
>CG51099-03
MGRWCQTVARGQRPRTSAPSRAGALLLLLLLLLRSAGCWGAGEAPGALSTADPADQSVQCV   60
PKATCPSSRPRLLWQTPTTQTLPSTTMETQFPVSEGKVDPYRSCGFSYEQDPTLRDPEAV   120
ARRWPWMVSVRANGTHICAGTIIASQWVLTVAHCLIWRDVIYSVRVGSPWIDQMTQTASD   180
VPVLQVIMHSRYRAQRFWSWVGQANDIGLLKLKQELKYSNYVRPICLPGTDYVLKDHSRC   240
TVTGWGLSKADGMWPQFRTIQEKEVIILNNKECDNFYHNFTKIPTLVQIIKSQMMCAEDT   300
HREKFCYELTGEPLVCSMEGTWYLVGLVSWGAGCQKSEAPPIYLQVSSYQHWIWDCLNGQ   360
ALALPAPSRTLLLALPLPLSLLAAL                             385 (SEQ ID NO:49)
```

Figure 20. Nucleotide and Protein Sequences For CG57051-04.

Nucleotide sequence encoding the Angiopoietin-like protein, CG57051-04.

>CG57051-04
TGCGGATCCTCACACGACTGTGATCCGATTCTTTCCAGCGGCTTCTGCAACCAAGCGGGT 60
CTTACCCCCGGTCCTCCGCGTCTCCAGTCCTCGCACCTGGAACCCCAACGTCCCCGAGAG 120
TCCCCGAATCCCCGCTCCCAGGCTACCTAAGAGGATGAGCGGTGCTCCGACGGCCGGGGC 180
AGCCCTGATGCTCTGCGCCGCCACCGCCGTGCTACTGAGCGCTAGATCTGGACCCGTGCA 240
GTCCAAGTCGCCGCGCTTTGCGTCCTGGGACGAGATGAATGTCCTGGCGCACGGACTCCT 300
GCAGCTCGGCCAGGGGCTGCGCGAACACGCGGAGCGCACCCGCAGTCAGCTGAGCGCGCT 360
GGAGCGGCGCCTGAGCGCGTGCGGGTCCGCCTGTCAGGGAACCGAGGGGTCCACCGACCT 420
CCCGTTAGCCCCTGAGAGCCGGGTGGACCCTGAGGTCCTTCACAGCCTGCAGACACAACT 480
CAAGGCTCAGAACAGCAGGATCCAGCAACTCTTCCACAAGGTGGCCCAGCAGCAGCGGCA 540
CCTGGAGAAGCAGCACCTGCGAATTCAGCATCTGCAAAGCCAGTTTGGCCTCCTGGACCA 600
CAAGCACCTAGACCATGAGGTGGCCAAGCCTGCCCGAAGAAAGAGGCTGCCCGAGATGGC 660
CCAGCCAGTTGACCCGGCTCACAATGTCAGCCGCCTGCACCGAGGCTGGTGGTTTGGCAC 720
CTGCAGCCATTCCAACCTCAACGGCCAGTACTTCCGCTCCATCCCACAGCAGCGGCAGAA 780
GCTTAAGAAGGGAATCTTCTGGAAGACCTGGCGGGGCCGCTACTACCCGCTGCAGGCCAC 840
CACCATGTTGATCCAGCCCATGGCAGCAGAGGCAGCCTCCTAGCGTCCTGGCTGGGCCTG 900
GTCCCAGGCCCACGAAAGACGGTGACTCTTGGCTCTG 937 (SEQ ID NO:50)

Protein sequence encoded by the nucleotide sequence shown above.

>CG57051-04
MSGAPTAGAALMLCAATAVLLSARSGPVQSKSPRFASWDEMNVLAHGLLQLGQGLREHAE 60
RTRSQLSALERRLSACGSACQGTEGSTDLPLAPESRVDPEVLHSLQTQLKAQNSRIQQLF 120
HKVAQQQRHLEKQHLRIQHLQSQFGLLDHKHLDHEVAKPARRKRLPEMAQPVDPAHNVSR 180
LHRGWWFGTCSHSNLNGQYFRSIPQQRQKLKKGIFWKTWRGRYYPLQATTMLIQPMAAEA 240
AS 242 (SEQ ID NO:51)

Figure 21. Nucleotide and Protein Sequences For CG57051-05.

Nucleotide sequence encoding the Angiopoietin-like protein, CG57051-05.

```
>CG57051-05
CTTCGTCTCCAGTCCTCGCACCTGGAACCCCAACGTCCCCGAGAGTCCCCGAATCCCCGC     60
TCCCAGGCTACCTAAGAGGATGAGCGGCGCTCCGACGGCCGGGGCAGCCCTGATGCTCTG    120
CGCCGCCACCGCCGTGCTACTGAGCGCTCAGGGCGGACCCGTGCAGTCCAAGTCGCCGCG    180
CTTTGCGTCCTGGGACGAGATGAATGTCCTGGCGCACGGACTCCTGCAGCTCGGCCAGGG    240
GCTGCGCGAACACGCGGAGCGCACCCGCAGTCAGCTGAGCGCGCTGGAGCGGCGCCTGAG    300
CGCGTGCGGGTCCGCCTGTCAGGGAACCGAGGGGTCCACCGACCTCCCGTTAGCCCCTGA    360
GAGCCGGGTGGACCCTGAGGTCCTTCACAGCCTGCAGACACAACTCAAGGCTCAGAACAG    420
CAGGATCCAGCAACTCTTCCACAAGGTGGCCCAGCAGCAGCGGCACCTGGAGAAGCAGCA    480
CCTGCGAATTCAGCATCTGCAAAGCCAGTTTGGCCTCCTGGACCACAAGCACCTAGACCA    540
TGAGGGTGGCAAGCCTGCCCGAAGAAAGAGGCTGCCCGAGATGGCCCAGCCAGTTGACCC    600
GGCTCACAATGTCAGCCGCCTGCACCATGGAGGCTGGACAGTAATTCAGAGGCGCCACGA    660
TGGCTCAGTGGACTTCAACCGGCCCTGGGAAGCCTACAAGGCGGGGTTTGGGGATCCCCA    720
CGGCGAGTTCTGGCTGGGTCTGGAGAAGGTGCATAGCATCATGGGGGACCGCAACAGCCG    780
CCTGGCCGTGCAGCTGCGGGACTGGGATGGCAACGCCGAGTTGCTGCAGTTCTCCGTGCA    840
CCTGGGTGGCGAGGACACGGCCTATAGCCTGCAGCTCACTGCACCCGTGGCCGGCCAGCT    900
GGGCGCCACCACCGTCCCACCCAGCGGCCTCTCCGTACCCTTCTCCACTTGGGACCAGGA    960
TCACGACCTCCGCAGGGACAAGAACTGCGCCAAGAGCCTCTCTGGAGGCTGGTGGTTTGG   1020
CACCTGCAGCCATTCCAACCTCAACGGCCAGTACTTCCGCTCCATCCCACAGCAGCGGCA   1080
GAAGCTTAAGAAGGGAATCTTCTGGAAGACCTGGCGGGGCCGCTACTACCCGCTGCAGGC   1140
CACCACCATGTTGATCCAGCCCATGGCAGCAGAGGCAGCCTCCTAGCGTCCTGGCTGGGC   1200
CTGGTCCCAGGCCCACGAAAGAGGTGACTCTTGGCTCTG     1239 (SEQ ID NO:52)
```

Protein sequence for Angiopoietin-like protein, CG57051-05.

```
>CG57051-05
MSGAPTAGAALMLCAATAVLLSAQGGPVQSKSPRFASWDEMNVLAHGLLQLGQGLREHAE     60
RTRSQLSALERRLSACGSACQGTEGSTDLPLAPESRVDPEVLHSLQTQLKAQNSRIQQLF    120
HKVAQQQRHLEKQHLRIQHLQSQFGLLDHKHLDHEGGKPARRKRLPEMAQPVDPAHNVSR    180
LHHGGWTVIQRRHDGSVDFNRPWEAYKAGFGDPHGEFWLGLEKVHSIMGDRNSRLAVQLR    240
DWDGNAELLQFSVHLGGEDTAYSLQLTAPVAGQLGATTVPPSGLSVPFSTWDQDHDLRRD    300
KNCAKSLSGGWWFGTCSHSNLNGQYFRSIPQQRQKLKKGIFWKTWRGRYYPLQATTMLIQ    360
PMAAEAAS    368   (SEQ ID NO:53)
```

Figure 22. Nucleotide and Protein Sequences For CG57051-02.

Nucleotide sequence encoding the Angiopoietin-like protein of the invention.

```
>CG57051_02
TGCGGATCCTCACACGACTGTGATCCGATTCTTTCCAGCGGCTTCTGCAACCAAGCGGGT    60
CTTACCCCCGGTCCTCCGCGTCTCCAGTCCTCGCACCTGGAACCCCAACGTCCCCGAGAG   120
TCCCCGAATCCCCGCTCCCAGGCTACCTAAGAGGATGAGCGGTGCTCCGACGGCCGGGGC   180
AGCCCTGATGCTCTGCGCCGCCACCGCCGTGCTACTGAGCGCTAGATCTGGACCCGTGCA   240
GTCCAAGTCGCCGCGCTTTGCGTCCTGGGACGAGATGAATGTCCTGGCGCACGGACTCCT   300
GCAGCTCGGCCAGGGGCTGCGCGAACACGCGGAGCGCACCCGCAGTCAGCTGAGCGCGCT   360
GGAGCGGCGCCTGAGCGCGTGCGGGTCCGCCTGTCAGGGAACCGAGGGGTCCACCGACCT   420
CCCGTTAGCCCCTGAGAGCCGGGTGGACCCTGAGGTCCTTCACAGCCTGCAGACACAACT   480
CAAGGCTCAGAACAGCAGGATCCAGCAACTCTTCCACAAGGTGGCCCAGCAGCAGCGGCA   540
CCTGGAGAAGCAGCACCTGCGAATTCAGCATCTGCAAAGCCAGTTTGGCCTCCTGGACCA   600
CAAGCACCTAGACCATGAGGTGGCCAAACCTGCCCGAAGAAAGAGGCTGCCCGAGATGGC   660
CCAGCCAGTTGACCCGGCTCACAATGTCAGCCGCCTGCACCATGAGGCTGGACAGTAAT   720
TCAGAGGCGCCACGATGGCTCAATGGACTTCAACCGGCCCTGGGAAGCCTACAAGGCGGG   780
GTTTGGGGATCCCCACGGCGAGTTCTGGCTGGGTCTGGAGAAGGTGCATAGCATCACGGG   840
GGACCGCAACAGCCGCCTGGCCGTGCAGCTGCGGGACTGGGATGGCAACGCCGAGTTGCT   900
GCAGTTCTCCGTGCACCTGGGTGGCGAGGACACGGCCTATAGCCTGCAGCTCACTGCACC   960
CGTGGCCGGCCAGCTGGGCGCCACCACCGTCCCACCCAGCGGCCTCTCCGTACCCTTCTC  1020
CACTTGGGACCAGGATCACGACCTCCGCAGGGACAAGAACTGCGCCAAGAGCCTCTCTGC  1080
CCCATCGGTGGCTCAAAGACCTGACCATGTTCCCTCTCCCCTGACCCCGGCAGGAGGCTG  1140
GTGGTTTGGCACCTGCAGCCATTCCAACCTCAACGGCCAGTACTTCCGCTCCATCCCACA  1200
GCAGCGGCAGAAGCTTAAGAAGGGAATCTTCTGGAAGACCTGGCGGGGCCGCTACTACCC  1260
GCTGCAGGCCACCACCATGTTGATCCAGCCCATGGCAGCAGAGGCAGCCTCCTAG    1315
(SEQ ID NO:54)
```

Protein sequence for CG57051-02.

```
>CG57051_02
MSGAPTAGAALMLCAATAVLLSARSGPVQSKSPRFASWDEMNVLAHGLLQLGQGLREHAE    60
RTRSQLSALERRLSACGSACQGTEGSTDLPLAPESRVDPEVLHSLQTQLKAQNSRIQQLF   120
HKVAQQQRHLEKQHLRIQHLQSQFGLLDHKHLDHEVAKPARRKRLPEMAQPVDPAHNVSR   180
LHHGGWTVIQRRHDGSMDFNRPWEAYKAGFGDPHGEFWLGLEKVHSITGDRNSRLAVQLR   240
DWDGNAELLQFSVHLGGEDTAYSLQLTAPVAGQLGATTVPPSGLSVPFSTWDQDHDLRRD   300
KNCAKSLSAPSVAQRPDHVPSPLTPAGGWWFGTCSHSNLNGQYFRSIPQQRQKLKKGIFW   360
KTWRGRYYPLQATTMLIQPMAAEAAS    386    (SEQ ID NO:55)
```

Figure 23. Nucleotide and Protein Sequences For CG57051-03.

Nucleotide sequence encoding the Angiopoietin-like protein, CG57051-03.

```
>CG57051-03
CCCCGAGAGTCCCCGAATCCCCGCTCCCAGGCTACCTAAGAGGATGAGCGGTGCTCCGAC      60
GGCCGGGGCAGCCCTGATGCTCTGCGCCGCCACCGCCGTGCTACTGAGCGCTCAGGGCGG     120
ACCCGTGCAGTCCAAGTCGCCGCGCTTTGCGTCCTGGGACGAGATGAATGTCCTGGCGCA     180
CGGACTCCTGCAGCTCGGCCAGGGGCTGCGCGAACACGCGGAGCGCACCCGCAGTCAGCT     240
GAGCGCGCTGGAGCGGCGCCTGAGCGCGTGCGGGTCCGCCTGTCAGGGAACCGAGGGGTC     300
CACCGACCTCCCGTTAGCCCCTGAGAGCCGGGTGGACCCTGAGGTCCTTCACAGCCTGCA     360
GACACAACTCAAGGCTCAGAACAGCAGGATCCAGCAACTCTTCCACAAGGTGGCCCAGCA     420
GCAGCGGCACCTGGAGAAGCAGCACCTGCGAATTCAGCATCTGCAAAGCCAGTTTGGCCT     480
CCTGGACCACAAGCACCTAGACCATGAGGTGGCCAAGCCTGCCCGAAGAAAGAGGCTGCC     540
CGAGATGGCCCAGCCAGTTGACCCGGCTCACAATGTCAGCCGCCTGCACCATGGAGGCTG     600
GACAGTAATTCAGAGGCGCCACGATGGCTCAGTGGACTTCAACCGGCCCTGGGAAGCCTA     660
CAAGGCGGGGTTTGGGGATCCCCACGGCGAGTTCTGGCTGGGTCTGGAGAAGGTCCATAG     720
CATCACGGGGGACCGCAACAGCCGCCTGGCCGTGCAGCTGCGGGACTGGGATGACAACGC     780
CGAGTTGCTGCAGTTCTCCGTGCACCTGGGTGGCGAGGACACGGCCTATAGCCTGCAGCT     840
CACTGCACCCGTGGCCGGCCAGCTGGGCGCCACCACCGTCCCACCCAGCGGCCTCTCCGT     900
ACCCTTCCCCACTTGGGACCAGGATCACGACCTCCGCAGGGACAAGAACTGCGCCAAGAG     960
CCTCTCTGGAGGCTGGTGGTTTGGCACCTGCAGCCATTCCAACCTCAACGGCCAGTACTT    1020
CCGCTCCATCCCACAGCAGCGGCAGAAGCTTAAGAAGGGAATCTTCTGGAAGACCTGGCG    1080
GGGCCGCTACTACCCGCTGCAGGCCACCACCATGTTGATCCAGCCCATGGCAGCAGAGGC    1140
AGCCTCCTAG    1150 (SEQ ID NO:56)
```

Protein sequence for CG57051-03.

```
>CG57051-03
MSGAPTAGAALMLCAATAVLLSAQGGPVQSKSPRFASWDEMNVLAHGLLQLGQGLREHAE      60
RTRSQLSALERRLSACGSACQGTEGSTDLPLAPESRVDPEVLHSLQTQLKAQNSRIQQLF     120
HKVAQQQRHLEKQHLRIQHLQSQFGLLDHKHLDHEVAKPARRKRLPEMAQPVDPAHNVSR     180
LHHGGWTVIQRRHDGSVDFNRPWEAYKAGFGDPHGEFWLGLEKVHSITGDRNSRLAVQLR     240
DWDDNAELLQFSVHLGGEDTAYSLQLTAPVAGQLGATTVPPSGLSVPFPTWDQDHDLRRD     300
KNCAKSLSGGWWFGTCSHSNLNGQYFRSIPQQRQKLKKGIFWKTWRGRYYPLQATTMLIQ     360
PMAAEAAS    368 (SEQ ID NO:57)
```